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SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name:Phone		_ Examiner # :	Date:	
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lease provide a detailed statement of the neclude the elected species or structures, tility of the invention. Define any terms nown. Please attach a copy of the cover	keywords, synonyms, act s that may have a special	onyms, and registry numbe meaning. Give examples or	rs, and combine with the co	ncept or
itle of Invention:				
nventors (please provide full names):				
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For Sequence Searches Only* Please incli			issued patent numbers) along	with the
ppropriate serial number.	-			
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Listing first 45 summaries
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opyright (c) 1993 - 2003 Compugen Ltd.

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Full length wild t
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              17-JUN-1997;
(IMMV ) IMMUNEX CORP
                                         12-JUN-1998;
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                                                              23-DEC-1998
                                                                                   WO9857655-A1
                                                                                                       Homo sapiens
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                                                                                                                                                                                                                                  AAW67769 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             screened with a fragment corresponding to the extracellular domain of mouse flt3 ligand (flt3-L) (nt 103-516 of AAQ79076) to isolate human flt3-L cDNA. Flt-3 stimulates progenitor and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure;
                                                                                                                                                Antigen-specific peripheral immune tolerance; flt3-ligand; flt3-L;
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tissue transplantation.
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                                                                                                                                                                                                   cancer; dendritic cell; immune re
myelodysplasia; aplastic anemia;
multiple myeloma; leukemia.
                                                                                                                                                                                                                                                                                     Immunomodulator; immunosuppressive; cytostatic; antianemic; anti-HIV; neuroprotective; antiallergic; flt3 ligand; flt3-L; wild type; allergy; cell surface tyrosine kinase receptor; hematopoletic progenitor cell; cellular expansion; cellular differentiation; natural killer cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Full length wild type human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A method has been developed of initiating or enhancing: (i) an antigen-
specific immune tolerance; or (ii) immunotolerance of a therapeutic
immunogenic molecule by addition of a polypeptide, before, after or with
the mucosal administration of an immunotolerising amount of the antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 standard;
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                                                                                                                                                                                                                                                                   immune response;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 1242; DB ZU;
Pred. No. 5e-109;
                                                                                                                                                                                                                                  HIV infection; lymphoma; neuroblastoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antigen specific
an flt3 ligand
                                                                                                                                                                                                                                                                   autoimmunity;
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13-JAN-2000

Homo

sapiens

99WO-US14296

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AAB2012 4
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                                                                                                                                                                                                                                                                                                            В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to novel soluble flt3 ligand (flt3-L) polypeptides which exhibits increased or decreased biological activity relative to the full length wild type (this sequence) or mature (AANS9720) flt3-L polypeptides. The flt3-L protein binds cell surface tyrosine kinase receptors and regulate growth and differentiation of hematopoietic progenitor cells. The flt3-L protein can be used to induce cellular capacitally in vivo) or differentiation of hematopoietic expansion (especially in vivo) or differentiation, e.g. 'ln'.') the mematopoietic, natural killer (NK) or dendritic cells, especially in the presence of growth factors such as interlepkins, colony stimulating. Capacitors or protein kinases. The protein fanglase modulate, augment or enhance a patient's immune response and can be used to treat an immune disorder (e.g. allergy, autoimmunity or immunosuppression). The protein may be used to treat a pathological condition e.g. myslodysplasia. The protein capacitic anemia, HTV infection, breast, small cell lung, testicular or ovarian cancer, lymphoma, multiple mysloma, 'neuroblastoma or acute'.
AAB20192 standard; Protein; 235 AA.

AAB20192;

AAB20192;

T 14-MAY-2001 (first entry)

X

E Human Flt-3 ligand.

E Human Flt-3 ligand; Fms-like tyrosine kinase; human; waccine; melanoma; giloma; W inmunotherapy; therapy; tumour; cancer; melanoma; giloma; W lymphoma; autoimmune disease; infection; gene therapy.

KX

Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Sim
Matches 235;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mutant soluble flt3 ligand polypeptide used in cellular expansion, immune response stimulation or treatment of pathological conditions contains amino acid substitutions at positions 8, 84, 118 or 122 - Claim 1; Page 72-73; 90pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Graddis TJ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                              ASNLQDEELCGGLWRLVLAQRWMERLKTVAGSKMQGLLERVNTETHFVTKCAFQPPPSCL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 1242, DB 21, Length 235, 100.0%; Pred. No. 5e-109; tive 0; Mismatches, (0) Indels 0; Gaps
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                                                                                                                                                                                                                 The present sequence is that of human Fms-like tyrosine kinase (Flt-3 ligand). The invention is directed to enhancing the immune response of a vertebrate to an antigen or a cytokine by administering in vivo, into a tissue of a vertebrate, a Flt-3 ligand-encoding polynucleotides, and 1 or more antigen- or cytokine-encoding polynucleotides. The Flt-3 ligand-encoding polynucleotides are nicely folynucleotide may encode the present full-length human Flt-3 cytopy for the ligand. The polynucleotides are incorporated into the cells of the vertebrate in vivo, and a prophylactically or therapeutically effective amount of Flt-3 ligand and 1 or more antigens or cytokines is produced in vivo. Pharmaceutical compositions comprising the polynucleotides are useful for suppressing tumour growth in a mammal. The tumour is melanoma, glioma or lymphoma, particularly B-cell lymphoma. They can also be used for the prophylactic and/or therapeutic treatment of:

(a) bacterial (e.g. Bacillus infections), viral (e.g. hepatitis B and C in humans), parasitic (e.g. malaria) and fungal infections; (b) autoimmune diseases (e.g. rhemmatoid arthritis B and osteoarthritis); (c) cancer; and (d) Aujeszky's disease in pigs. Various other examples of these diseases are given in the
                                                                                                                    Matches
                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Immunogenic compositions comprising Flt-3 ligand encoding polynucleotide and one or more antigen, or cytokine encoding polynucleotides, useful for suppressing tumour growth and for autoimmune diseases (e.g. rheumatoid arthritis)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Domain
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                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 2; Page 132-133; 149pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-JUL-1999;
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                                                                         1 MTVLAPAWSPTTYLLLLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTV
2001-123319/13.
DB; AAF30310.
                                                           MTVLAPAWSPTTYLLLLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTV
                                                                                                                   11 Similarity 100 235; Conservative
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                                                                                                                                                                               AA;
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183..205
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27..182
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27..235
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                                                                                                                    0;
                                                                                                                   Score 1242; DB 22
Pred. No. 5e-109;
; Mismatches 0;
                                                                                                                                                  22;
                                                                                                                    Indels
                                                                                                                                              Length
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121

RFVQTNISRLLQETSEQLVALKPWITRQNFSRCLELQCQPDSSTLPPPWSPKPLEATAPT

180

δÃ 멍 20 DЪ Q

Вb

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RESULT 5
ABB08129
                                                                                                                                                      PT antigen-specific T cells -

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Disclosure; Page 37-38; 43pp; English.

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CC

CF of invention relates to treating an individual at risk for or suffering convergence of involves administering a combination of two to the agents compositions of convolves administering a combination of two to the agents compositions (c) dendritic cell mobilisation factor; (b) dendritic cell maturation agent; (c) dendritic cell activation agent; (d) The dell anthurcing factor; (c) agent; (e) activated, antigen-specific T cells. The methods are useful for treating an individual at risk for or suffering from infection with a pathogenic or opportunistic organism, and the conversion of the cell agents of cell. In the cell agent which causes chaga's disease). The methods are especially centancing a lymphocyte-mediated immune response. In particular, the method is useful for treating inflammations, chickenpox, oral or genital herpes, mononucleosis, multifocal leukoencephalopathy, hepatitis, AIDS, cell leukemia or T cell lymphoma. The activated antigen-presenting cell dendritic cells are useful as a vaccine adjuvant. The present sequence cerpresents a human FIL3L polypeptide fragment, that can be used as a cell dendritic cell mobilisation factor.
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PN

MO200236141-A2.

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10-MAY-2002.

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20-CCT-2001; 2001WO-US44834.

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O2-NOV-2000; 2000US-245721P.

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CLynch DH, De Smedt TN, Maliszewski CR, Butz EA, Miller RE PI Thomas EK;

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YX

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Treating an individual suffering from infection, e.g. inflammation, PT Treating an individual suffering from infection, e.g. inflammation, PT Thomas or AIDS, by administering a combination of dendritic cell PT mobilization factor or maturation agent T cell enhancing factor and PT antigen-specific T cells -

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Discocurs. Page 37-30.
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b 181 APOPPILLLLLPVGLLLAAAWCLHWORTERRIPREGOVPPVPSPODLLVEH 235

b 181 APOPPILLLLLPVGLLLAAAWCLHWORTERRIPREGOVPPVPSPODLLVEH 235

NBB08129

RESULT 5

NBB08129 standard; protein; 235 AA.

CX ABB08129; XX

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Mmna Flt3L polypeptide.

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Dendritic cell; mobilisation factor; T cell; adjuvant; antibacterial; KW fungicide; protozoacide; virucide; anti-inflammatory; anti-HIV.

XX

XX

Muman Flt3L polypeptide.

XX

XX

Muman Flt3L cell; mobilisation factor; T cell; adjuvant; antibacterial; KW fungicide; protozoacide; virucide; anti-inflammatory; anti-HIV.

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XX

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Homo sapiens.
                                                                             Matches
                                                                                               Query Match
Best Local
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                                                                                                                                                      Sequence
                                                                            thes 235;
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                   1 MTVLAPAWSPTTYLLLLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPYTV 60
MTVLAPAWSPTTYLLLLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTV 60
                                                                            h 100.0%;
Similarity 100.0%;
35; Conservative
                                                                                                                                                      AA;
                                                                            0;
                                                                        Score 1242; DB 23; Length 235; Pred. No. 5e-109; Mismatches 0; Indels 0;
                                                                Indels; 0;
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ARACE ARACE
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BOS
HUMBA
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ARACE
PF 18-M
PF 19-M
PR 13-A
PR 119-M
PR 13-A
PR 13-
                                            A cDNA library from the human stromal cell line 295V48, in pME185, was screened with an 800 bp fragment derived from mouse clone T118. This fragment encompasses the coding region conserved between two mouse clones, T118 and T110. Approx. 20 positive clones were selected and partially sequenced. Two clones, S86 and S109, were found to be approx. 75% homologous to the mouse clones over the first 163 AAs. Clone S86 continued to show homology to T110 until the stop codon, although to a lesser degree, for an overall homology of 66%. Clones T18 and S109 do not show homology to each other or to the other clones after mouse residue 163 (human residue 160). An additiona mouse clone designated MB8 has a 29 AA insert at the junction between the common and divergent portions of the mouse ligand.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19-MAY-1993;
07-JUL-1993;
16-JUL-1993;
13-AUG-1993;
24-AUG-1993;
19-NOV-1993;
03-DEC-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New ligand for the Flt3 tyrosine kinase receptor - and renucleic acid, vectors, host cells and antibodies, useful treating abnormal cell physiology and proliferation, e.g. also for diagnosis and drug screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (INRM
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Birnbaum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24-NOV-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              W09426891-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-AUG-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Page 76-77; 90pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tyrosine kinase receptor ligand
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93US-0089263.
93US-0092549.
93US-0106340.
93US-0112391.
93US-0155111.
93US-0162413.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and related
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Sequence

Query Match

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                         Claim 2; Page 137-138; 149pp; English.
                                    Immunogenic compositions comprising Flt-3 ligand encoding polynucleotide and one or more antigen, or cytokine encoding polynucleotides, useful for suppressing tumour growth and for autoimmune diseases (e.g. rheumatoid arthritis)
                                                                                                                                                                                                                                                                                                                Flt-3 ligand; Fms-like tyrosine kinase; human; vaccine; immunotherapy; therapy; tumour; cancer; melanoma; gliona; lymphoma; autoimmune disease; infection; gene therapy.
   The present sequence (Flt-3 ligand). The
                                                                                                                                                          31-JUL-2000; 2000WO-US20679
                                                                                                                                                                                                                    Domain
                                                                                                                                                                                                                                                                    Protein
                                                                                                                                                                                                                                                                                            Key
                                                                                                                                                                                                                                                                                                                                                          Human Flt-3 ligand.
                                                                                                                                                                                                                                                                                                                                                                        14-MAY-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                          AAB20194;
                                                                                                                                                                                                                                                                                                                                                                                                         AAB20194 standard; Protein;
                                                                                   N-PSDB;
                                                                                                                                            30-JUL-1999;
                                                                                                                                                                           08-FEB-2001
                                                                                                                                                                                            WO200109303-A2
                                                                                                                                                                                                                                    Domain
                                                                                                                                                                                                                                                    Domain
                                                                                                            Hermanson
                                                                                                                           (VICA-) VICAL
                                                                                                                                                                                                                                                                                    Peptide
                                                                                                                                                                                                                                                                                                           Homo sapiens.
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hes 234;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2001-123319/13.
DB; AAF30312.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APQPPLLLLLLPVGLLLLAAAWCLHWQRTRRRTPRPGEQVPPVPSPQDLLLVEH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ASNLQDEELCGGLWRLVLAQRWMERLKTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                            99US-0146170
                                                                                                                                                                                                                   /label
206..2
                                                                                                                                                                                                                                                   /label=
27..182
                                                                                                                                                                                                                                                                   /label= Signal_peptide
27..235
                                                                                                                                                                                                                                           /label=
                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                           /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99.5%;
99.6%;
   invention is
           is that
                                                                                                                                                                                                         Cytoplasmic_domain
                                                                                                                                                                                                                          Transmembrane_domain
                                                                                                                                                                                                                                           Extracellular_domain
                                                                                                                                                                                                                                                          Mature_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1236; DB 16;
Pred. No. 1.8e-108;
                                                                                                                                                                                                                                                                                                                                                                                                         235
           of human Fms-like tyrosine
                                                                                                                                                                                                                                                                                                                                                                                                         Å
   directed
                                                                                                                                                                                                                                                                                                                                                                                                         to enhancing
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è kinase
The
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cc administering in vivo, into a tissue of a vertebrate, a Flt-3 cc ligand-encoding polynucleotide, and 1 or more antigen or cytokine-encoding polynucleotides. The Flt-3 ligand-encoding Cc cytokine-encoding polynucleotides. The Flt-3 ligand-encoding Cc ligand polypeptide, or amino acids 27-185, 1-185, 27-235 or 1-235 cc ligand polypeptide, or amino acids 27-185, 1-185, 27-235 or 1-235 cc of the Flt-3 ligand. The polynucleotides are incorporated into Cc the cells of the vertebrate in vivo, and a prophylactically or cc therapeutically effective amount of Flt-3 ligand and 1 or more cc antigens or cytokines is produced in vivo. Pharmaceutical compositions comprising the polynucleotides are useful for suppressing tumour growth in a mammal. The tumour is melanoma, Cc glioma or lymphoma, particularly B-cell lymphoma. They can also be used for the prophylactic and/or therapeutic treatment of:

(a) bacterial (e.g. Bacillus infections), viral (e.g. hepatitis B and contains), parasitic (e.g. malaria) and fungal infections; cb used cin humans), parasitic (e.g. malaria) and fungal infections; costeoarthritis); (c) cancer; and (d) Aujeszky's disease in pigs. Contains other examples of these diseases are given in the
Sequence
  235
  AA;
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Query Match
Best Local S
Matches 234
MTVLAPAMSPTTYLLLLLLLSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTV 60
                                                   Similarity
                                        99.5%;
nilarity 99.6%;
Conservative
                                          0;
                                        Score 1236; I
Pred. No. 1.8e
0; Mismatches
                                                  DB 22;
                                                          Length
                                         0
                                        Gaps
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61 61 ASNLQDEELCGGLWRLVLAQRWMERLKTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSCL 120 ASNLQDEELCGALWRLVLAQRWMERLKTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSCL

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- Š 밁 121 121 RFVQTNISRLLQETSEQLVALKPWITRQNFSRCLELQCQPDSSTLPPPPWSPRPLEATAPT RFVQTNISRLLQETSEQLVALKPWITRQNFSRCLELQCQPDSSTLPPPWSPRPLEATAPT 180 180
- Ω 181 APOPPLLLLLLLPVGLLLLAAAWCLHWQRTRRRTPRPGEQVPPVPSPQDLLLVEH 235
- 밁 181 **APQPPLLLLLLLPVGLLLLAAAWCLHWQRTRRRTPRPGEQVPPVPSPQDLLLVEH**

AAY69721 standard; Protein;

ĄΑ

AAY69721;

05-JUL-2000 (first entry)

Human flt-3 mutein L-3H

cell surface tyrosine kinase receptor; hematopoietic progenitor cell; cellular expansion; cellular differentiation; natural killer cell; cancer; dendritic cell; immune response; autoimmunity; immunosuppression; myelodysplasia; aplastic anemia; HIV infection; lymphoma; neuroblastoma; multiple myeloma; leukemia; mutein. neuroprotective; cell surface tyro Immunomodulator; immunosuppressive; cytostatic; antianemic; anti-HIV; neuroprotective; antiallergic; flt3 ligand; flt3-L; wild type; allerg ; allergy; or cell;

Homo sapiens Synthetic.

WO200001823-A2

25-JUN-1999; 99WO-US14296

98US-0109100

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RESULT 9
AAW69007
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to novel soluble flt3 ligand (flt3-L) polypeptides CC which exhibits increased or decreased biological activity relative to CC the full length wild type (AAY69719) or mature (AAY69720) flt3-L CC polypeptides. This sequence represents an example of the novel fit-3 CC ligands and comprises the L-3H mutant polypeptide. The flt3-L protein CC binds cell surface tyrosine kinase receptors and regulate growth and CC differentiation of hematopoietic progenitor cells. The flt3-L protein can CC be used to induce cellular expansion (especially in vivo) or dendritic CC cells, especially in the presence of growth factors such as interleukins, CC colony stimulating factors or protein kinases. The protein can also CC modulate, augment or enhance a patient's immune response and can be used to treat an immune disorder (e.g. allergy, autoimmunity or condition e.g. myelodysplasia, aplastic anemia, HIV infection, breast, can mail cell lung, testicular or ovarian cancer, lymphoma, multiple CC myeloma, neuroblastoma or acute leukemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
Matches 211
                                                                      Human; flt-3 receptor agonist; haematopoietic cell stimulation; cancer; bone marrow reconstitution; haematological disease; immune deficiency; drug-induced myelosuppression; renal dialysis; gene therapy; infection; congenital metabolic disease; neurological disease; therapy;
                                                                   congenital metabolic dendritic cell produc
                                                                                                                                                       Human flt-3
                                                                                                                                                                                 01-OCT-1998
                                                                                                                                                                                                                                       AAW69007 standard; peptide; 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 4; Page 79-80; 90pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mutant soluble flt3 ligand polypeptide used in cellular expansion, immune response stimulation or treatment of pathological conditions contains amino acid substitutions at positions 8, 84, 118 or 122
             WO9818923-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                               182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      85
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                                                                                                                                                                                                                                                             LHWQRTRRRTPRPGEQVPPVPSPQDLLLVEH 235
                                                                                                                                                                                                                                                                                                                                                                  SGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPYTVASNLQDEELCGGLWRLVLAQRWME 84
                                       sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                          RLKTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSCLRFVQTNISRLLQETSEQLVALKPN 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              212 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                     receptor agonist.
                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90.5%; Score 1124, DB 21; Length 21279 100.0%; Pred. No. 5.9e-98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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     -1- 42
-1- 42
-1- 42
-1-
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Mature wild

human flt-3

protein

05-JUL-2000 (first entry)

AAY69720 standard;

Protein;

ΑA

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RESULT 10
AAY69720
ID AAY69
XX
AC AAY69
XX
DT 05-JU
XX
DE Matur
XX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CC cells in vivo (e.g. in a subject about to donate blood) or for ex vivo (expansion for subsequent transplantation, e.g. to reconstitute bone (c) marrow after chemotherapy, disease etc., or to treat haematological (disease such as drug-induced myelosuppression, defects caused by infections, burns or renal dialysis. Optionally ex vivo expanded cells (c) are transduced with a gene therapy vector for treating e.g. congenital metabolic diseases, immune deficiency, neurological disease, cancer and (c) infections. The agonists can also be used in the treatment of tumours, (c) infections and autoimmune disease, when administered optionally with an artigen. The agonist can also be used in the production of dendritic cells for use as an immunising adjuvant for treatment disorders including acquired immune deficiency syndrome. Compared with native ligands, the convergence of the conv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Feng Y, Mo
Staten NR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence represents a rearranged human flt-3 receptor agonists the invention. The agonists have a modified flt-3 ligand amino acid sequence. The agonists are used to stimulate production of haematopo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rearranged flt-3 receptor agonists and nucleic used to stimulate production of haematopoietic for treatment of haematological diseases, bone and in gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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                                                                                                                                                                                                                                                                          181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         RONFSRCLELQCOPDSSTLPPPWSPRPLEATAPTAPQPPLLLLLLLPVGLLLLAAAWCLH
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R, Streeter PR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        209 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 89.7%; Score 1114; DB 19; 100.0%; Pred. No. 5.1e-97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             McWherter
R, Woulfe
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                                                                                                                                                                                                                                                                                                                               Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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                                        207
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                                                                                                                                                                                                                                                   TQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASNLÓDEELCGGLWRLVLAQRWMERL
                                                                                                                                                                             KTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSCLRFVQTNISRLLQETSEQLVALKEWIT 146
                                                                                                                                                                                                                                 TQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASNLQDEELCGGLNRLVLAQRWMERL
  WQRTRRTPRPGEQVPPVPSPQDLLLVEH
                    WQRTRRRTPRPGEQVPPVPSPQDLLLVEH
                                                                                              RQNFSRCLELQCQPDSSTLPPPWSPRPLEATAPTAPQPPLLLLLLLLLPVGLLLLAAAWCLH
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                                                                            RQNFSRCLELQCQPDSSTLPPPWSPRPLEATAFTAPQPPLLLLLLLPVGLLLLADAWCLH 180
                                                                                                                                                    KTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSCLRFVQTNISR;LQETS@QLVALKEWIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Page 89-90; 90pp; English.
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                                                                                                                                                                                                                                                                                                       89.7%; Score 1114; DB 21; Length 209; llarity 100.0%; Pred. No. 5.1e-97; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  acid
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209 · ;
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                                                                                                                                                                              Matches
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immune
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 4; Page 84-85; 90pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Graddis TJ, McGrew JT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
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                                                                                                                                                                                                                                                     Sequence
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147
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                                                                                                                                                                                                Local
                                                  KTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSCLRFVQTNISRLLQETSEQLVALKPWIT
                                                                                                                         TQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASNLQDEELCGGLWRLVLAQRWMERL
                                                                                                      TQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASNLQDEELCGGLWRLVLAQRWMERL
RQNFSRCLELQCQPDSSTLPPPWSPRPLEATAPTAPQPPLLLLLLLPVGLLLLAAAWCLH
                                 KTVAGSKMQGLLERVNTEIHFVTECAFQPPPSCLRFVQTNISRLLQETSEQLVALKPWIT
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                                                                                                                                                                              208;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             soluble flt3 ligand polypeptide used in cellular expansion, response stimulation or treatment of pathological conditions ns amino acid substitutions at positions 8, 84, 118 or 122 -
                                                                                                                                                                            Similarity 99.9
08; Conservative
                                                                                                                                                                                                                                                                                        neuroblastoma or
                                                                                                                                                                                                                                                     209 AA;
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1; Mis
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No. 1.2e-96;
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RESULT 12
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                                                                                                                                                                                                                                                                 The invention relates to novel soluble flt3 ligand (flt3-L) polypeptides which exhibits increased or decreased biological activity relative to the full length wild type (AAY69719) or mature (AAY69720) flt3-L propertides. This sequence represents an example of the novel flt-3 colligands and comprises the Q122R mutant polypeptide. The flt3-L protein binds cell surface tyrosine kinase receptors and regulate growth and colligands and comprises the Q122R mutant polypeptide. The flt3-L protein can be used to induce cellular expansion (especially in vivo) or dendritic collis. The flt3-L protein can be used to induce cellular expansion (especially in vivo) or cells, especially in the presence of growth factors such as interleukins, colony stimulating factors or protein kinases. The protein can also modulate, augment or enhance a patient's immune response and can be used to treat an immune disorder (e.g. allergy, autoimmunity or immunosuppression). The proterin may be used to treat a pathological condition e.g. myelodysplasia, aplastic anemia, HIV infection, breast, consultations, neuroblastoma or acute leukenia.
                                                                                                    Query Match
Best Local
                                                                     Matches
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                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 4; Page 88-89; 90pp; English.
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27 TQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASNLQDEELCGGLWRLVLAQRWMERL
                                                                                                 Local
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mo sapiens.
nthetic.
200001823-A2.
-JAN-2000.
-JUN-1999; 99WO-US14296.
-JUL-1998; 98US-0109100.

MMY ) IMMUNEX CORP.
addis TJ, McGrew JT;
I; 2000-182115/16.
I; 2000-182115/16.
tant soluble flt3 ligand polypeptide used in cellular expansion, mune response stimulation or treatment of pathological conditions ntains amino acid substitutions at positions 8, 84, 118 or 122 -
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                                                                                                 Similarity
                                                                                                                                                                                                                                                        neuroblastoma or
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                                                                        Conservative
                                                                                                 89.4%;
99.5%;
                                                                                                                                                                                                                                                        acute leukemia.
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                                                                 Score'1110; D
Pred. No. 1.2e
1; Mismatches
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                                                                                    DB 21; Length 209; .2e-96;
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RESULT 13
AAY69727
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The invention relates to novel soluble flt3 ligand (flt3-L) polypeptides which exhibits increased or decreased biological activity relative to CC the full length wild type (AN469719) or mature (AN469720) flt3-L CC polypeptides. This sequence represents an example of the novel flt-3 CC ligands and comprises the L26F mutant polypeptide. The flt3-L protein CC binds cell surface tyrosine kinase receptors and regulate growth and CC differentiation of hematopoietic progenitor cells. The flt3-L protein can be used to induce cellular expansion (especially in vivo) or CC differentiation, e.g. in hematopoietic, natural killer (NK) or dendritic cells, especially in the presence of growth factors such as interleukins, CC colony stimulating factors or protein kinases. The protein can also CC modulate, augment or enhance a patient's immune response and can be used to treat an immune disorder (e.g. allergy, autoimmunity or condition e.g. myelodysplasia, aplastic anemia, HTV infection, breast, condition e.g. myelodysplasia, aplastic anemia, HTV infection, breast,
                                                                                                                                                                                                                                                                                                                                                    Mutant soluble flt3 ligand polypeptide used in cellular expansion, immune response stimulation or treatment of pathological conditions contains amino acid substitutions at positions 8, 84, 118 or 122 -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Immunomodulator; immunosuppressive; cytostatic; antianemic; anti-HTV; neuroprotective; antiallergic; flt3 ligand; flt3-L; wild type; allergy; cell surface tyrosine kinase receptor; hematopoletic progenitor cell; cellular expansion; cellular differentiation; natural killer cell;
                                                                                                                                                                                                                                                                                                                Claim 13; Page 82-83; 90pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cancer; dendritic cell; immune response; autoimmunity; immunosuppression;
myelodysplasia; aplastic anemia; HIV infection; lymphoma; neuroblastoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (IMMV ) IMMUNEX CORP
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The invention relates to novel soluble flt3 ligand (flt3-L) polypeptides which exhibits increased or decreased biological activity relative to the full length wild type (AAY69719) or mature (AAY69720) flt3-L polypeptides. This sequence represents an example of the novel flt-3 ligands and comprises the L26F mutant polypeptide. The flt3-L protein binds cell surface tyrosine kinase receptors and regulate growth and differentiation of hematopoietic progenitor cells. The flt3-L protein cal
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Mutant soluble flt3 ligand polypeptide used in cellular expansion, immune response stimulation or treatment of pathological condition contains amino acid substitutions at positions 8, 84, 118 or 122

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Pred. No. 1.9e
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US-09-109-100-17
US-09-109-100-15
US-08-243-545-2
US-08-243-545-2
US-08-27-109-100-19
US-08-27-109-100-19
PCT-US94-05365-2
US-09-109-100-19
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PCT-US94-05365-2
US-09-109-100-19
PCT-US94-05365-2
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US-08-993-962-6
US-09-160-841-6
            US-08-317-522A-9
US-08-439-818A-9
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US-08-243-545-6
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ALIGNMENTS

Sequence 6, Application US/08243545
Patent No. 5554512
GENERAL INFORMATION: TELEX: 756822 INFORMATION FOR SEQ ID NO: ETLING DATE: August 12, 11
CLASSIPICATION 435
PRIOR APPLICATION DATA:
APPLICATION UMBER: 08/066
ETLING DATE: May 24, 1993
CLASSIPICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Malaska, Stephen L. FILING DATE: 11-MAY-1S
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 03-DEC-15
APPLICATION AUMBER: 05
FILING DATE: August 25 REFERENCE/DOCKET NUMBER: 28
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430 CURRENT APPLICATION DATA: APPLICATION NUMBER: US APPLICANT: Lyman, Stewart D.
APPLICANT: Beckmann, M. Patricia
TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors SEQUENCE CHARACTERISTICS CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: COMPUTER READABLE FORM: MEDIUM TYPE: Floppy CORRESPONDENCE ADDRESS: NUMBER OF SEQUENCES: CITY: STATE: COMPUTER: Apple Macintosh OPERATING SYSTEM: Macintos TELEFAX: REGISTRATION NUMBER: SOFTWARE: Microsoft Word, COUNTRY: STREET: LENGTH: ADDRESSEE: 98101 AGENT INC....
Malaska, Stephen L.
Malaska, Stephen L.
2,655 Seattle Washington 51 University (206) 233-0644 SD Stephen L. amino acids NUMBER: 08/106,463 August 12, 1993 May 24, 1993)N: 435 NUMBER: 08/111,758 August 25, 1993 Floppy disk UMBER: US/08/243,545 11-MAY-1994 JMBER: US 08/162,407 03-DEC-1993 Macintosh 7.0.1 08/068,394 Malaska, Immunex Corporation Street 6. 2813-C Version #5.1

TYPE: am:

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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                     CLASSIFICATION DATA:
PRIOR APPLICATION NUMBER: US/08/162,407
                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                    CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                         CLASSIFICATION: 424
PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
NUMBER OF SEQUENCES: 8
                              TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: Macintosh 7.0.1 SOFTWARE: Microsoft Word, Version
                                                                 NAME: Malaska, Stephen L. REGISTRATION NUMBER: 32,6
                                                                                                                   FILING DATE: M. CLASSIFICATION:
                                                                                                                                                                                                      APPLICATION NUMBER: 08/106,4
FILING DATE: August 12, 1993
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TELEFAX:
            TELEPHONE:
                                                REFERENCE/DOCKET NUMBER:
                                                                                                                                                      APPLICATION NUMBER:
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FILING DATE: August 25, 1993
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                (206)
                                                                                                                                  May 24, 1993
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                                                                                                                                                                                                                                                                                                               December 3,
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ER: 2813-C
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Pred. No. 1
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, MOLECULE TYPE: protein US-08-993-962-6
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US-09-160-841-6
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GENERAL INFORMATION:
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REFERENCE/DOCKET NUMBER: 28
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/106,463
FILING DATE: August 12, 1993
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MEDIUM TYPE: Floppy disk
                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Microsoft Word, Version CURRENT APPLICATION DATA:
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                                                                                      FILING DATE: May 24, 1993 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Beckmann, M. Patricia
TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
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                                                    REGISTRATION NUMBER:
                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                   FILING DATE: Decembre APPLICATION NUMBER:
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mes 235; Conserv
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JUMBER: 08/111,758
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; TYPE: PRT
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US-09-109-100-1
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CURRENT FILING DATE: 1998-07-02
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
Sequence 6, Application PC/TUS9405365 GENERAL INFORMATION:
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Best Local
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APPLICANT: McGrew, Jeffrey T.
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS
FILE REFERENCE: 03260.0028
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SEQUENCE CHARACTERISTICS
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Pred. No. 1.7e-117;
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LENGTH: 235 amino acids
TYPE: amino acid
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TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
NUMBER OF SEQUENCE: 8
CORRESPONDENCE ADDRESS:
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APPLICATION NUMBER:
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CITY: Seattle
121 RFVQTNISRLLQETSEQLVALKPWITRQNFSRCLELQCQPDSSTLPPPWSPRPLEATAPT 180
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                                                61 ASNLQDEELCGGLWRLVLAQRWMERLKTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSCL 120
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CLASSIFICATION:
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FILING DATE: August 12,
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OPERATING SYSTEM: PC-DOS/MS-DOS
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March 7, 1994
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RESULT 7
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SEQ ID NO 18
LENGTH: 209
TYPE: PRT
ORGANISM: Homo sapiens
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CURRENT FILING DATE: 1998-07-02
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 10
LENGTH: 212
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Patent No. 6291661
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                                                        Matches 209;
                                                                                              Query Match
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                                                                                                                                                                                                                                                 APPLICANT: Graddis, Thomas J.
APPLICANT: MCGTCW, Jeffrey T.
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS
FILE REFERENCE: 03260.0028
CURRENT APPLICATION NUMBER: US/09/109,100C
CURRENT FILING DATE: 1998-07-02
NUMBER OF SEQ ID NOS: 20
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APPLICANT: McGrew, Jeffrey T.
TITLE OF INVENTION: FLT3-L MUTANTS
FILE REFERENCE: 03260.0028
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                                                        Local Similarity 100.
hes 209; Conservative
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                                                                          89.7%; Score 1114; DB 4; 100.0%; Pred. No. 1.2e-104;
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                                                                                              DB 4; Length 209;
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; SEQ ID NO 12
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-109-100-12
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US-09-109-100-12
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APPLICANT: Graddis, Thomas J.
APPLICANT: McGrew, Jeffrey T.
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 9
LENGTH: 209
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Best Local Similarity
                                                                                 CURRENT APPLICATION NUMBER: US/09/109,100C
CURRENT FILING DATE: 1998-07-02
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                     APPLICANT: Graddis, Thomas J.
APPLICANT: McGrew, Jeffrey T.
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS
FILE REFERENCE: 03260.0028
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Pred. No. 3e-104;
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Best Local Sim
Matches 208;
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LENGTH: 20
                                                                           GENERAL INFORMATION:
                                                                                         Sequence 17, Application US/09109100C Patent No. 6291661
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APPLICANN: MCGrew, Jeffrey T.
APPLICANN: MCGrew, Jeffrey T.
FILE OF INVENTION: FLT3-L MUTANTS AND MET:
FILE REFERENCE: 03260.0028
CURRENT APPLICATION NUMBER: US/09/109,100C
CURRENT FILING DATE: 1998-07-02
NUMBER OF SEQ ID NOS: 20
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin Ver. 2.1
                       APPLICANT: Graddis, Thomas J.
APPLICANT: McGrew, Jeffrey T.
TITLE OF INVENTION: FLT3-L MUTANTS AND NETHODS
FILE REFERENCE: 03260.0028
CURRENT APPLICATION NUMBER: US/09/109,100C CURRENT FILING DATE: 1998-07-02
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Pred. No. 3e-104;
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Pred. No. 3e-104;
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RESULT 13
US-09-109-100-15
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US-09-109-100-11
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SEQ ID NO 11
LENGTH: 209
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Matches 208; Conserv
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LENGTH: 209
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Best Local
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Best Local Similarity
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APPLICANT: McGrew, Jeffrey T.
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS
FILE REFERENCE: 03260.0028
CURRENT APPLICATION NUMBER: US/09/109,100C
CURRENT FILING DATE: 1998-07-02
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin Ver. 2.1
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SOFTWARE: Patentin
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TYPE: PRT
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Pred. No. 3e-104;
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Pred. No. 4.8e-104;
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Sequence 15, Application Patent No. 6291661

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LENGTH: 209
TYPE: PRT
ORGANISM: Homo sapiens
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-109-100-13
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SOFTWARE: PatentIn Ver.
SEQ ID NO 13
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Matches 208; Conserv
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CURRENT FILING DATE: 1998-07-02
NUMBER OF SEQ ID NOS: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Graddis, Thomas J.
APPLICANT: McGrew, Jeffrey T.
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS
FILE REFERENCE: 03260.0028
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APPLICANT: McGrew, Jeffrey T.
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
FILE REFERENCE: 03260.0028
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Pred. No. 4.8e-104;
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; ORGANISM: Homo sapiens
US-09-109-100-8
Search completed: May 27, Job time : 17 secs
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Best Local Similarity
Matches 208; Conserv
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SEQ ID NO 8
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APPLICANT: McGrew, Jeffrey T.

TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
FILE REFERENCE: 03260.0028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/109,100C CURRENT FILING DATE: 1998-07-02
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                                                         WQRTRRRTPRPGEQVPPVPSPQDLLLVEH 235
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Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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1242
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sp_bacteria:*
sp_fungi:*
sp_human:*
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sp_unclassified:*
sp_rvirus:*
sp_bacteriap:*
sp_archeap:*
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sp_phage:*
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sp_virus:*
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668
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  6 Q9MZU9
6 Q9GKE9
6 Q9GKE9
6 Q9GKNW1
6 Q9GKD9
11 Q61104
11 Q8UCH4
10 Q9LGG8
5 Q9GY13
5 Q9GY33
11 Q8UYM6
5 Q9GY33
11 Q9DWH8
10 Q9C5T0
5 Q17889
11 Q8VD70
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O9mzv0 canis famil
O9mzu9 felis silve
O9gke0 bos taurus
O8wnw1 bos taurus
O9gkd9 bos taurus
O9gkd9 bos taurus
O9l104 mus musculu
O8vch4 mus musculu
O9l9g8 oryza sativ
O9l9g1 leishmania
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O9vim6 mus musculu
O9n753 leishmania
O9c5t0 arabidopsis
O17889 caenorhabdi
O8vd70 mus musculu
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	45	44	43	42	41	40	39	38	37	36	<u>3</u>	34	ω	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17
	85	85	85	85	85.5	86	86	86	86	86.5	87	87	• "	87.5	88	88	88	88.5	88.5	88.5	88.5	88.5	89.5	90.5	90.5	90.5	92	92.5	92.5
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,	Q9p2d0 homo sapien	Q99mm1 mus musculu	Q9a3k1 caulobacter	Q9bsal homo sapien	Q95uq2 toxoplasma	O35407 mus musculu		Q84647 paramecium	Q9d3j3 mus musculu		Q8ta74 hemicentrot	_				Q9dbt2 mus musculu	Q9gke2 sus scrofa		Q943d5 oryza sativ	Q9awj4 oryza sativ	-	Q8ywx3 anabaena sp	O17610 caenorhabdi	Q9pu36 gallus gall	_	Q9gya0 leishmania	Q9had2 homo sapien	Q8szs7 drosophila	Q9gyal leishmania

ALIGNMENTS

Qy	Db x	0	Дb	Qy	Ma Be	SQ	DR	DR	DR	RL	RT	RT	RT	RA	RX	RР	RN	o x	8	8	SO	DE	DT	DT	DŢ	AC	ID	RESULT Q9MZV0
121 RFVQTNISRLLQETSEQLVALKPWITRQNFSRCLELQCQPDSSTLPPPWSPRPLEATAPT 180		61 ASNLODEELCGGLWRLVLAORWMERLKTVAGSKMOGLLERVNTEIHFVTKCAFOPPPSCL 120	1 MIVLAPAWSPTASLLLLLLLSPGLRGTPDCSFSHSPISSTFAVTIRKLSDYLLQDYPVTV 60	1 MTVLAPAMSPTTYLLLLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTV 60	Query Match 72.1%; Score 895.5; DB 6; Length 294; Best Local Similarity 77.1%; Pred. No. 3.5e-80; Matches 182; Conservative 12; Mismatches 35; Indels 7; Gaps 3;	SEQUENCE 294 AA; 32394 MW; 6859917A3B74ABCD CRC64;	Pfam; PF02947; flt3_lig; 1.	InterPro; IPR004213; Flt3_lig.	EMBL; AF155148; AAF87088.1;	DNA Seq. 11:163-166(2000).	long cytoplasmic domain.";	degree of similarity to the human and mouse homologue but uniquely	"Molecular cloning of canine and feline flt3 ligand reveals high	Yang S., Sim G.K.;	MEDLINE=20358731; PubMed=10902925;	SEQUENCE FROM N.A.				Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Canis familiaris (Dog).		21,	(TrEMBLrel. 15,	(TrEMBLrel.	~-	Q9MZVO PRELIMINARY; PRT; 294 AA.	TIT 1

Qy Db

181

APQPP-LLLLLLPVGLLLLAAAWCLHW-QRTRRRTPRPGEQVPPVPS-----PQD

RFVQTNISHLLQDTSQQLAALKPWITRRNFSGCLELQCQPDSSTLVPPRSPGALEATALP 180

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Best Local S
Matches 178
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Q9GKEO;
01-MAR-2001 (TrEMBLrel.
01-MAR-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Molecular cloning of canine and feline fit3 ligand reveals high degree of similarity to the human and mouse homologue but uniquely long cytoplasmic domain.";

DNA Seq. 11:163-166(2000).

EMBL; AF155149; AAP87089.1;

FIRM: IPR004213; FIt3_lig.

Pfam; PF02947; flt3_lig: 1.

SEQUENCE 291 AA; 32459 MW; 8F85A10A5EAODCC6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-2000 (TrEMBLrel. 01-OCT-2000 (TrEMBLrel. 01-JUN-2002 (TrEMBLrel. Flt3 ligand.
Nwanqi W., Brown W.C., Palmer G.H.; "Identification of fetal liver tyrosine kinase 3 (Flt3) ligand domain required for receptor binding and function using naturally occurring ligand isoforms.";
                                                                                              SEQUENCE FROM N.A.
MEDLINE=20570936; PubMed=11120823;
                                                                                                                                                                                                    Bos taurus (Bovine).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;

Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                     01-DEC-2001
Flt3 ligand
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
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Last sequence update)
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Q8WNW1;
Q1-MAR-2002 (TrEMBLrel. 2
01-MAR-2002 (TrEMBLrel. 2
01-JUN-2002 (TrEMBLrel. Elt3 ligand.
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EMBL; AF282985; AAF99322.1; -.
InterPro: IPR004213; F1t3_119.
Pfam; PF02947; f1t3_119; 1.
SEQUENCE 292 AA; 32390 MW; D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hikono H., Momotani E.;
"Cloning of a CDNA for bovine flt3 ligand.";
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ
EMBL; AB051841; BAB79634.1; -.
Interpro; IPR004223; Flt3_lig.
Pfam; PF02947; flt3_lig. 1.
SEQUENCE 292 AA; 32388 MW; 2A797E0C1199CIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pe
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NCBI_TaxID=9913;
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PGPQSPLLLLLLLLPVALLLLATAWCLCRWRRRRRTRYPGER
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75.9%;
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224
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Best Local S
Matches 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mwangi W., Brown W.C., Palmer G.H.;
"Identification of fetal liver tyrosine kinas required for receptor binding and function us ligand isoforms.";
J. Immunol. 165:6966-6974(2000).
EMBL; AF282986; AAR99323.1;
InterPro; IPR004213; Flt3_lig.
pfam; pF02947; flt3_lig; 1.
SEQUENCE 274 AA; 30372 MW; 725A7F77A95DA9
                                                                                                                                                                                                                       Q61104
Q61104;
Q1-NOV-1996
Q1-NOV-1996
Q1-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9GKD9;
Q9GKD9;
01-MAR-2001
01-MAR-2001
01-DEC-2001
Flt3 ligand
                                          "Flt3 ligand: expression, ge forms and processing "; Submitted (DEC-1995) to the EMBL; U44024; AAA93305.1; MGD; MGI:95560; Flt31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrat
Mammalia; Eutheria; Cetartiodactyla; Ruminantia;
Bovidae; Bovinae; Bos.
                                                                                                 SEQUENCE FROM N.A.
MCClanahan T., Culpepper J.,
Mattson J., Tsai S., Luh J.,
Birnbaum D., Hannum C.;
                                                                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                        Mus musculus (Mouse)
           InterPro; IPR004213; Flt3_lig.
InterPro; IPR001230; Prenyl_site.
Pfam; PF02947; flt3_lig; 1.
                                                                                                                                                        NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE=20570936; PubMed=11120823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9913;
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AR-2001 (TrEMBLrel. 16,
EC-2001 (TrEMBLrel. 19,
llgand isoform-2.
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156; Conser
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                                                                                                                                                                  Chordata;
Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     %; Score 746; DB
%; Pred. No. 1.8e
12; Mismatches
                                                                                       genomic
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Last sequence up
                                                                                                                                                                                                                       Created)
Last sequence update)
Last annotation updat
                                                                                                          Campbell
Guimares
                                                                  EMBL/GenBank/DDBJ
                                                                                                                                                                  Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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                                                                                       organization,
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                                                                                                           М. J., W
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minantia; Pecora;
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cora; Bovoidea;
                                                                                                          Franz-Bacon
.-G., Rosnet
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RESULT
Q9LGG8
        ON COORDINATED NO COO
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Q8VCH4
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Best Local S
Matches 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best
O9LGGB;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence up
01-UN-2002 (TrEMBLrel. 21, Last annotation
putative extensin-like protein.
p0406H10.6 OR O11174_D05.5.

Oryza sativa (Rice).
Eukaryota; Viridiplantae; Streptophyta; Embr
Spermatophyta; Magnoliophyta; Liliopsida; Pc
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (DEC-2001) to the EMEL BC019801; AAH19801.1; -. EMBL; BC019801; F18004213; F113_lig. Pfam; PF02947; f1t3_lig; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2002 (TrEMBLrel. 20, 01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                        Q9LGG8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Strausberg R.;
Submitted (DEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-LIVER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse)
Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similar to FMS-like tyrosine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   <u>س</u>
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                                                                                                                                                                                                                                                                                                                                                                                                                                 LREVQTNISRLLQETSEQLVALKPWITR--QNESRCLELQCQPDSSTLPPPWSPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LRFVQTNISHLLKDTCTQLLALKPCIGKACQNFSRCLE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VASNLQDEELCGGLWRLVLAQRWMERLKTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MTVLAPAWSPNSSLLLLLLLLSPCLRGTPDCYFSHSPISSNFKVKFRELTDHLLKDYPVT
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122; Conser
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                                                                                                                                                                                                                                          PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18986 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19465 MW;
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Last annotation update)
e kinase 3 ligand.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 578; DB 11;
Pred. No. 3.7e-49;
4; Mismatches 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 602.5;
Pred. No. 1.
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Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                          PRT;
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                                                Embryophyta; Trach
a; Poales; Poaceae;
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                                                                 Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                168
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Best Local S
Matches 54
                                                                                                                                                                                                                                                                  Q9GY11;
                     Submitted (AUG-2001) to the EMBL/GenBank/DDBJ EMBL; AL390114; CAC02038.2; -. InterPro; IPR000561; EGF-like. InterPro; IPR001511; LRR. InterPro; IPR001595; P_rich_extensn. Pfam; PF00560; LRR; 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PR01582; KV33CHANNEL.
PRINTS; PR01217; PRICHEXTENSN.
SMART; SM00370; LRR; 5.
PROSITE; PS00030; LRR; Type 1; UNKNOWN 1.
PROSITE; PS00030; RRM_RNP_1; UNKNOWN 1.
SEQUENCE 579 AA; 62607 MW; 04457E18E7405AAF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Oryza sativa nipponbare(GA3) genomic clone:0J1174_D05.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [1]
SEQUENCE FROM N.A.
STRAIN=CV. NIPPONBARE;
Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, clone:P0406H10.";
                                                                                                                                                                                                                             01-MAR-2001 (TrEMBLrel. 16, 01-OCT-2001 (TrEMBLrel. 18, 01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases EMBL; AP002524; BAB07956.1; .. EMBL; AP003118; BAB33013.1; ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=CV. NIPPONBARE;
Sasaki T., Matsumoto T.,
SMART;
                                                                                                   Oliver K.;
                                                                                                            Murphy L., Quail M., Harris D.,
                                                                                                                           STRAIN=FRIEDLIN;
                                                                                                                                                                            Leishmania major.
Eukaryota; Euglen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted
          PRINTS;
                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                Probable surface antigen
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                                                                                                                                                                NCBI_TaxID=5664;
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InterPro; IPR000504; RNA_rec_mot.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001611; LRR.
                                                                                                                                                                                                                                                                                                                                               392
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                                                                                                                                                                                                                                                                                                                                               PSPPPP---
                                                                                                                                                                                                                                                                                                                                                                      TAPQPPLLLLLLPVGLLLLAAAWCLHWQRTRRRTPRPGEQVPPVPSP
                                                                                                                                                                                                                                                                                                                                                                                                            NI--SRLLQETSEQLVALKPWITRQNFSR----CLELQCQPDSSTLPPPWSPRPLEATAP 179
                                                                                                                                                                                                                                                                                                                                                                                                                                              VAGMRKVEOL-DVAHNLLTGAIPQAVCELPRLKNFTFAYNFFTGEPPSCAHAVPRYGDRR 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASNLQDEELCGGLWRL 76
                                                                                                                                                                                                                                                                                                                                                                                               NCLPNRPAQRTLRQCAAF-----FARPPVNCAAFQCKPFVPALPPPSPPPP--SPPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VLAQRWMERLKTVAGSKMQGLLERVNTEIHFVTKCAFQ-----PPPSCLRFV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PF00560; LRR;
SM00181; EGF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 54;
          PR01217;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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                                                                                                                                                                            Euglenozoa; Kinetoplastida;
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                                                                                                                                                                                                                                                                                 PRELIMINARY;
          PRICHEXTENSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9.1%;
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                                                                                                                                                                                                                 p2
                                                                                                                                                                                                                              Last sequence up
                                                                                                                                                                                                                                                      Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 112.5; DB 10; Pred. No. 0.013;
                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                               -----SPPPSTSPPPSP
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                                                                                                              Rajandream
                                                                                                                                                                                                                                                                                 668
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                                                                                                                                                                            Trypanosomatidae;
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                                                                                      databases
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                                                                                                               Barrell
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RESULT 10
Q9GY33
RESULT
Q8VIM6
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Best Local
                                                                                                                                                                                                                                                 Matches
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9GY33;
Q9GY33;
Q1-MAR-2001;
01-OCT-2001;
01-JUN-2002;
                                                                                                                                                                                                                                                                                                            Pfam; PF00560; LRR; 7.
PRINTS; PR01217; PRICHEXTENSN
SMART; SM00181; EGF; 1.
                                                                                                                                                                                                                                                                                                                                                                       Submitted (AUG-2001) to the EMBL; AL390114; CAC02017.2; InterPro; IPR000561; EGF-1i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Leishmania major.
Eukaryota; Euglenozoa;
NCBI_TaxID=5664;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                             Murphy L., Quail M., Oliver K.;
                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                InterPro;
                                                                                                                                                                                                                                                                                                                                                            InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-FRIEDLIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LM12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Probable surface antigen
                                                                                                                                                 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        119
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                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 LAPAWSPTTYLLLLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DSSTLPPPWSPR-----PLEATAPTAPQPP------LLLLLLLPVGLL--LLAAAW 203
                                                                      DSSTLPPPWSPR-----PLEATAPTAPQPP-----LLLLLLLPVGLL--LLAAAW
                                                                                                                                                                                                                        LAPAWSPTTYLLLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASN 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VSGTLPPEWSSMGSLANLQLSLTQVSGTLPPQWSSMRKLTQLLLTDTLLSGTLPAEW 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLRFVQ---TNISRLLQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LPPEWSSMPNLQTLQVRRLKLSGT-----LPADWS-SLKSLSNVVLEDMPIT----
                                                                                                                      CLRFVQ---TNISRLLQ----
                                                                                                                                                                        LQDEELCGGLWRLVLAQRWMERLKTVAGSKMQGLLERVNTEIHFVTKCAFQPPP-----S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALRELTLDGTNLSGTLPPQWSAMASVISLNLEGTEVSGTLPPKWISMSRL-QTLNLRRTK 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LQDEELCGGLWRLVLAQRWMERLKTVAGSKMQGLLERVNTEIHFVTKCAFQPPP----S
                                               VSGTLPPEWSSMGSLANLQLSLTQVSGTLPPQWSSMKKLTQLLLTDTLLSGTLPAEW
                                                                                                ALRFLTLDGTNLSGTLPPQWSAMASVISLNLEGTEVSGTLPPEWISMSRL-QTLNLRRTK 288
                                                                                                                                                 -----GL----LPPEW------
                                                                                                                                                                                                 LPPEWSSMPNLNAVELKRLKLSGT--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----GL----LPPEW-------GSLERIQQLVLRKLKLTGPLPPQWSPMK 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63;
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                                                                                                                                                                                                                                                                                                                                                             IPR001611; LRR.
                                                                                                                                                                                                                                                                                                648 AA;
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(TrEMBLrel. 18, 1
2 (TrEMBLrel. 21, 1
urface antigen p2.
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ilarity 26.6%;
Conservative 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA;
                                                                                                                                                                                                                                                                                                  68470 MW;
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                                                                                                                                                                                                                                                            8.3%;
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                                                                                                                                                                                                                                                                                                                                                P_rich_extensn
                                                                                                                                                                                                                                                                                                                                                                                                                       Harris D., Rajandream M., Ivens A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kinetoplastida;
                                                                                                                                                                                                                                                  20;
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                                                                                                                                                                                                                                               Score 102.5;
Pred. No. 0.14
20; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 104.5; DB Pred. No. 0.093;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CEB3ECAABC490C94 CRC64;
                                                                                                                                                                                                                                                                                                  8EB78AC101E01286 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                       ETSEQLVALKP-WITRQNFSRCLELQCQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ETSEQLVALKP-WITRONFSRCLELQCQP
                                                                                                                                                 -GSLERIQQLVLRKLKVTGPLPPQWSPMK 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   648
                                                                                                                                                                                                 -LPADWS-SLKSLSNVVLEDMPIT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Trypanosomatidae; Leishmania.
                                                                                                                                                                                                                                                              . 14;
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                                                                                                                                                                                                                                                                        DB 5;
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                                                                                                                                                                                                                                                  77;
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                                                                                                                                                                                                                                                                        Length 648;
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                                                                                                                                                                                                                                                  77;
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RESULT
Q9N753
ID V53
ID C53
AC Q6
DT 00
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Best Local S
Matches 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                            O9N753 PRELIMINARY;
O9N753;
O1-OCT-2000 (TrEMBLrel. 15, C:
O1-OCT-2001 (TrEMBLrel. 18, L;
O1-DEC-2001 (TrEMBLrel. 19, L;
Probable surface antigen p2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q8VIM6;
Q8VIM6;
01-MAR-2002
01-MAR-2002
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Mutations in a new gene encoding a protein of non-syndromic deafness at the DFNB16 locus."; Nat. Genet. 29:345-349(2001). EMBL; AF375593; AAAL35321.1; -. MGD; MGI:2153816; Strc.
SEQUENCE 1809 AA; 196404 MW; 012382C9E80EC8
   InterPro; IPR001611; LRR.
InterPro; IPR003592; LRR_out.
Pfam; PF00560; LRR; 3.
SMART; SM00370; LRR; 3.
                                                                                                                        Submitted (AUG-2001) to the EMBL; AL390114; CAB98658.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WEDLINE-21547528; PubMed-11687802;
Verpy E., Masmoudi S., Zwaenepoel I., Le
Del Castillo I., Mouaille S., Blanchard
Moreno F., Mueller R.F., Petit C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                       Murphy L., Quail M., Oliver K.;
                                                                                                                                                                                                                                                    STRAIN-FRIEDLIN
                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=5664;
                                                                                                                                                                                                                                                                                                                                                                   Leishmania major.
Eukaryota; Euglenozoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                        LM12.08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID-10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTPRPPPTTPQPPPTTTQPIP------DTTQPPPVTPRPPPTTPQPPPS 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AT---APTAPQPPLLLLLLLPVGLLLLAAAWCLHWQRTRRRTPRPGEQVP-PVPS 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRASQPAAHISP----RQRRAISVEALCENHSGPEPPYSISNFSIYLLCQHIKPATPRPPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QETSEQLVALKPWITRQNESRCLELQCQPDSSTLPP------PWSPRPLE
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Metazoa; Chordata; C
----heria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 (TrEMBLrel.
2 (TrEMBLrel.
2 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGSKMQGLLERVNTEIHFVTKC----AFQPPPSCLRFVQTNISRLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8.1%;
23.7%;
                                                                                                                                                                                                                    Harris
                                                                                                                                                                                                                                                                                                                                                                      Kinetoplastida; Trypanosomatidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20,
21,
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                                                                                                                                                                                                                 D.,
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 100.5;
Pred. No. 0.
                                                                                                                                                        EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation updat
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Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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                                                                                                                                                                                                                    Rajandream
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Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hutchin
                                                                                                                                                                                                                 Α.,
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                                                                                                                                                                                                                                                                                                                                                                Leishmania.
                                                                                                                                                                                                                    Barrell
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J.L.,
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Q9DWH8
ID Q1
AC Q1
DT 0:
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Best Local S
Matches 56
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Best Local :
Matches 2:
Q9C5T0;
Q9C5T0;
01-JUN-2001
01-JUN-2001
                                                                                                                                                                                                                                                    1113
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                                                                                                                                                                                                                                                                                                          202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Virol.
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01-MAR-2001
01-MAR-2001
01-DEC-2001
                                                                                                                                                                                                                                          "Rat cytomegalovirus R89 is spliced transcript."; Virus Res. 69:119-130(2000). EMBL; AF232689; AAF99111.1; SEQUENCE 1240 AA; 125612
                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-MAASTRICHT;
MEDLINE-20366325; PubMed-10906222;
                                                                                                                                                                                                                                                                                                               Gruijthuijsen Y.K.,
                                                                                                                                                                                                                                                                                                                             STRAIN=MAASTRICHT;
MEDLINE=20473137; PubMed=11018281;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Betaherpesvirinae;
NCBI_TaxID=79700;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rat cytomegalovirus (strain Maastricht)
Viruses; dsDNA viruses, no RNA stage; H
                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                              AWCLHWORTRRRTPRPGEQVPPVPSPQD
                                                                                                                         PDSSTL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LSRLPQPALRHRLN-----PQPPLRHRLNPRPLLP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SSTLPPPWSPRPLEATAPTAPQPPLLLLL----LLPVGLLLLAAAWCLHWQRTRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IHFVTKCAFQP----PPSCLRFVQTNISRLLQETSEQLVALKPWITRQNFSRCLELQCQPD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PEWGSMTSLSVLNLRGTGISGTLPPQWSGMSKARSLQLQDCDLSGSLPSSWSAI---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PAWSPTTYLLLLLLSSGLSGT-------QDCSFQHSPISSDFAVKIRELS
                                                                                                                                                                                   l Similarity
29; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -WLLRTAQRPPLSPPPRQRPPRTSLT--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  . Similarity 56; Conserv
                                                                                                                                                                                                                                                                                                                                                                                     Beuken E., Bruggeman C.A.
e DNA sequence of the rat
. 74:7656-7665(2000).
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nilarity 23.8%;
Conservative 2
                                                                  QATRASPRPETDAPP-PTPAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -PMLASVSLKGNKFCGVCRTRGIRRLVLL--WTSRTSTRAATA---
                                                                                                                                                                                    Conservative
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Muromegalovirus
                                                                                                                                           -----PPPWSPRP--LEATAPTAPQP-PLLLLLLLPVGLLLLAA
                                                                                                                                                                                                                                                                                                 Beuken E., Bruggeman C.A., R89 is a highly conserved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37530 MW;
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Pred. No. 0.17
21; Mismatches
                                                                                                                                                                                 Score 95.5; D
Pred. No. 1.5;
8; Mismatches
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Last annotation updat
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                                                                                                                                                                                                                                                                                                                                                                                                    cytomegalovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1240
658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Herpesviridae,
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I gene
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(TrEMBLrel.

17, 17,

Created)

sequence update)

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RESULT 15
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Best Local S
Matches 34
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InterPro; IPR002719; Euk_pkinase.
InterPro; IPR002719; Ser_thr_bkinase.
InterPro; IPR00229; Ser_thr_bkinase.
InterPro; IPR001245; Tyr_pkinase.
Pfam; PF01657; DUF26; 2.
Pfam; PF00069; Pkinase; 1.
ProDom; PD000001; Euk_pkinase; 1.
SMART; SM00219; S_TKC; 1.
SMART; SM00219; TyrKC; 1.
PROSITE; PS001107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
ATP-binding; Kinase; Transferase.
SEQUENCE 658 AA; 72991 MW; DCF9CF5F1748
                                                                                                                                                                                                                                                                                                                                                                                                                                    U1-JAN-1998 (TrEMBLrel. 0
01-JAN-1998 (TrEMBLrel. 0:
01-MAR-2002 (TrEMBLrel. 20:
F54F12.1 protein.
                                                                                                                                                                                                                                                                                                                                            Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Identification of genes encoding receptor-like protein kinases as possible targets of pathogen- and salicylic acid-induced WRKY DNA-binding proteins in Arabidopsis."; Plant J. 24:837-847(2000).
EMBL: AF224705; AAK28315.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                               SEQUENCE FROM N.A. MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       017889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. MEDLINE=20575726; PubMed=11135117:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2002 (TrEMBLrel. 20, Last annotation update) Receptor-like protein kinase 4.
EMBL;
                      investigating biology.";
Scienæe 282:2012-2018(1998).
                        Scienæe
                                                                                                      pone;
                                                                                                                                                                                                               Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                              Barlow
                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                            F54F12.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        138
                                                                          Genome sequence of the nematode
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Matches 38
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SEQUENCE
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SMART; SM00194; PTPc; 1.
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InterPro; IPR000387; TYR_phosphatase.
InterPro; IPR000242; Tyr_PP.
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                                                      GAVGGLLVVAIIGVILFFVFFQKKKKKEDKPDD--PPAPLP
                                                                                 LPVGLLLLAA-----AWCLHWQRTRRRTPRPGEQVPPVPSP 227
                                                                                                               ALRPQPTTSDPTAAAAPVPIPNNKGSLNGNPSPSSPPLLPPVASSTPAATPEESNMLLYII
                                                                                                                                       ALKPWITRQNESRCLELQCQPDSSTL---PPPWSPRPLEATAPTAP-----QPPLLLLLL 191
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Pred. No. :
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US-09-904-536-12

US-09-904-536-12

US-09-904-536-14

US-09-904-536-17

US-09-904-536-15

US-09-904-536-15

US-09-904-536-13

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US-09-220-920-26	US-10-001-054-56	US-09-220-920-52	US-10-001-873-50	US-09-223-490-4	US-09-783-708-1	US-09-925-300-1680	US-09-874-923-104	US-09-991-496-104	US-10-108-605-57	US-09-935-727-8	US-09-907-372-20	LO US-09-826-212-6	US-09-917-372-20	US-10-174-363-30	US-10-109-324-2	US-09-211-755B-47	US-09-818-879-47	US-10-300-616-31	US-09-793-139-47	US-09-826-508-26	US-09-899-471-5	US-09-863-818A-8	US-09-866-050A-509	US-09-899-471-2	US-09-904-536-19
Sequence 26, Appl	Sequence 56, Appl	Sequence 52, Appl	Sequence 50, Appl	Sequence 4, Appli	Sequence 1, Appl1	Sequence 1680, Ap	Sequence 104, App	Sequence 104, App	Sequence 57, Appl	8	Sequence 20, Appl	Sequence 6, Appli	20,	30	Sequence 2, Appli	Sequence 47, Appl	Sequence 47, Appl	Sequence 31, Appl	7, 1	Sequence 26, Appl	Sequence 5, Appli	Sequence 8, Appli	Sequence 509, App	N	Sequence 19, Appl

ALIGNMENTS

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US-10-095-449-6
Sequence 6, Application US/10095449
Patent No. US20020160004A1
GENERAL INFORMATION:
                                          APPLICATION NUMBER: 08/669,692
FILING DATE: 24-JUN-1996
APPLICATION NUMBER: US/08/162,407
FILING DATE: December 3, 1993
APPLICATION NUMBER: 08/111,758
FILING DATE: August 25, 1993
APPLICATION NUMBER: 08/165,463
APPLICATION NUMBER: 08/068,394
FILING DATE: August 12, 1993
APPLICATION NUMBER: 08/068,394
FILING DATE: May 24, 1993
ATTORNEY/ACENT INFORMATION:
REGISTRATION NUMBER: 32,655
REGEDENCE TOOCKET WITHERED 2813-C
REFERENCE/DOCKET NUMBER: 2813-C TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/095,449
APPLICATE: 13-Mar-2002
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Lyman, Stewart D.

Beckmann, M. Patricia
TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh 7.0.1
OPERATING SYSTEM: MacIntosh 7.0.1
SOFTWARE: Microsoft Word, Version
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SEQUENCE DESCRIPTION: SEQ ID NO: US-10-095-449-6
RESULT 3
US-09-983-806-6
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                                                                                                                                                                                                                                                                                                              Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US Patent No. US20020034517A1
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Best Local Similarity
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CURRENT FILING DATE: 1999-11-23
NUMBER OF SEQ ID NOS: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Brasel, Kenneth
TITLE OF INVENTION: Dendr:
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INFORMATION FOR SEQ
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                                                                                                                                                                                                                                   APQPPLLLLLLLPVGLLLLAAAWCLHWQRTRRRTPRPGEQVPPVPSPQDLLLVEH 235
                                                                                                                                    RFVQTNISRLLQETSEQLVALKPWITRQNFSRCLELQCQPDSSTLPPPWSPRPLEATAPT
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                                                                                                                                                                                                                                                                                           100.0%; ilarity 100.0%; Conservative 0;
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Pred. No. 1.4e-101;
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Pred. No. 1.4e-101;
; Mismatches 0;
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TYPE: amino acids

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO:
US-09-983-806-6
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Best Local Similarity
Matches 235; Conserv
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COMPUTER READABLE FORM:
MEDIUM TYPE: Flopp
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LENGTH: 235 amino acids
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TELEPHONE: (206) 587-0430
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Lyman, Stewart D. Beckmann, M. Patricia TITLE OF INVENTION: Ligands for NUMBER OF SEQUENCES: 8
APQPPLLLLLLLPVGLLLLAAAWCLHWQRTRRRTPRPGEQVPPVPSPQDLLLVEH 235
                                                                                                       RFVQTNISRLLQETSEQLVALKPWITRQNFSRCLELQCQPDSSTLPPPWSPRPLEATAPT 180
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                                                                                                                                                             ASNLQDEELCGGLWRLVLAQRWMERLKTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSCL
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                                                                                RFVQTNISRLLQETSEQLVALKPWITRQNFSRCLELQCQPDSSTLPPPWSPRPLEATAPT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/444,626
FILING DATE: 19-MAY-1995
APPLICATION NUMBER: US 08/162,407
FILING DATE: 03-DEC-1993
APPLICATION NUMBER: 08/111,758
FILING DATE: August 25, 1993
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FILING DATE: August 12, 193
APPLICATION NUMBER: 08/08,394
FILING DATE: May 24, 1993
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SEQ ID NO 10
LENGTH: 212
TYPE: PRT
ORGANISM: Homo sapiens
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LENGTH: 235
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APPLICANT: McGrew, Jeffrey T.
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
FILE REFERENCE: 02360.0028
CURRENT APPLICATION NUMBER: US/09/904,536
CURRENT FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: PRIOR APPLICATION: 09/109,100
PRIOR FILING DATE: 1999-07-02
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin Ver. 2.1
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NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn Ver. 2.1
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APPLICANT: McGrew, Jeffrey T.
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
FILE REFERENCE: 03260.0028
CURRENT APPLICATION UNMBER: US/09/904,536
CURRENT FILING DATE: 2001-07-16
PRIOR APPLICATION UNMBER: PRIOR APPLICATION: 09/109,100
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ORGANISM: Homo sapiens
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Local Similarity 100.0%; Pred. No. 3e-91;
hes 211; Conservative 0; Mismatches 0;
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US-09-904-536-18
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; ORGANISM: Homo sapiens
US-09-904-536-9
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APPLICANT: Graddis, Thomas J.
APPLICANT: McGrew, Jeffrey T.
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS
FILE REFERENCE: 03260.0028
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                                                                                                    CURRENT APPLICATION NUMBER: US/09/904,536
CURRENT FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: PRIOR APPLICATION: 09/109,100
PRIOR FILING DATE: 1999-07-02
NUMBER OF SEO ID NOS: 20
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CURRENT FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: PRIOR APPLICATION: 09/109,100
PRIOR FILING DATE: 1999-07-02
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin Ver. 2.1
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APPLICANT: McGrew, Jeffrey T.
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS
FILE REFERENCE: 03260.0028
                                                                                          SOFTWARE: PatentIn Ver.
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Local Similarity 100.0%; F
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                                                                           Sequence 14, Application US/09904536 Patent No. US20020111475A1 GENERAL INFORMATION:
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Best Local Similarity
Matches 208; Conserv
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SEQ ID NO 12
LENGTH: 209
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Best Local Similarity
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TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS
FILE REFERENCE: 03260.0028
                 FILE
                             APPLICANT: Graddis, Thomas J.
APPLICANY: McGrew, Jeffrey T.
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS
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CURRENT FILING DATE: 2001-07-16
 CURRENT
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APPLICATION NUMBER: US/09/904,536
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Best Local Similarity
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APPLICANT: McGrew, Jeffrey T.
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS
FILE REFERENCE: 03260.0028
CURRENT APPLICATION NUMBER: US/09/904,536
CURRENT FILING DATE: 2001-07-16
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PRIOR APPLICATION NUMBER: PRIOR APPLICATION: 09/109,100
PRIOR FILING DATE: 1999-07-02
NUMBER OF SEQ ID NOS: 20
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TYPE: PRT
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LENGTH: 209
TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                                      Query Match
Best Local 9
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SEQ ID NO 11
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TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS
FILE REFERENCE: 03260.0028
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APPLICANT: McGrew, Jeffrey T.
TITLE OF INVENTION: FLT3-FL MUTANTS AND METHODS
FILE REFERENCE: 03260.0028
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PRIOR APPLICATION NUMBER: PRIOR APPLICATION: 09/109,100
PRIOR FILING DATE: 1999-07-02
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TYPE: PRT
ORGANISM: Homo sapiens
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Pred. No. 7.4e-90;
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Pred. No. 7.4e-90;
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Best Local Similarity
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                                SEQ ID NO 8
LENGTH: 209
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APPLICANT: McGrew, Jeffrey T.
APPLICANT: MCGrew, Jeffrey T.
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
FILE REFERENCE: 03260.0028
CURRENT APPLICATION NUMBER: US/09/904,536
CURRENT FILING DATE: 2001-07-16
                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/904,536 CURRENT FILING DATE: 2001-07-16
                                                                                                                                                                                     APPLICANT: MCGrew, Jeffrey T. TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS
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TYPE: PRT
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ORGANISM: Homo sapiens
                  TYPE: PRT
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NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 16
LENGTH: 209
TYPE: PRT
ORGANISM: Homo sapiens
US-09-904-536-16
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Search completed: May 27, 2003, 18:36:27 Job time: 58 secs
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US-09-904-536-16
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Best Local Similarity 99.5%;
Matches 208; Conservative
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Best Local Similarity 99.5%;
Matches 208; Conservative
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CURRENT FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: PRIOR APPLICATION: 09/109,100
PRIOR FILING DATE: 1999-07-02
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TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF
FILE REFERENCE: 03260.0028
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Maximum Match 100%
Listing first 45 summaries
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TNR3_MOUSE
MPIP_DROWE
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ALIGNMENTS

This SWI between the Euro

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Best Local
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EMBL; U03858; AAA1982
EMBL; U29874; AAA90945
EMBL; U29874; AAA9095
PDB; 1ETE; 09 JUN-00.
                                                                           FL3L_MOUSE STANDARD; PRT; 232 AA. P49772; Q64085; 01-OCT-1996 (Rel. 34, Created) 01-OCT-1996 (Rel. 34, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) SL cytokine precursor (Fms-related tyrosine k ligand) (Flt3L).
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DISULFID
                      NCBI_TaxID=10090;
                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                    ligand) (Flt3L)
FLT3LG OR FLT3L
                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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Pfam; PF02947; flt3_lig; 1.
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MEDLINE=94195428;
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1316 OR FLISL.
Is musculus (Mouse).
"Parvota; Metazoa; Chordata; C
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                                                                                                                                                                                               APQPPLLLLLLPVGLLLLAAAWCLHWQRTRRRTPRPGEQVPPVPSPQDLLLVEH
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                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and this statement is not removed. Usage by and for commercial requires a license agreement (See http://www.isb-sib.ch/announce/
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AAA19825.1; -.
AAA90949.1; -.
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PubMed=8145851;
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N-LINKED (GLCNAC. . .) (POTENTIAL).
DSSTLPPWSPRPLEATA -> VETVFHRVSQDGLDLLTS
(IN ISOFORM 2).
MISSING (IN ISOFORM 2).
G -> A (IN REF. 1).
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Pred. No. 1.1
0; Mismatches
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                                      Craniata; Vert
Sciurognathi;
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Pro; IPR004213; Flt3_lig. PF02947; flt3_lig; 1.

Transmembrane;

Alternative splicing; Signal

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EMBL; U04807; AAA18000.1; -.
EMBL; L23636; AAA39436.1; -.
EMBL; U29875; AAA90951.1; -.
EMBL; U29875; AAA90952.1; -.
EMBL; S76459; AAB33069.1; -.
EMBL; S76461; AAB33070.1; -.
EMBL; S76464; AAB33071.1; -.
EMBL; S76464; AAB33071.1; -.
EMBL; U44024; AAA93307.1; -.
EMBL; U44024; AAA93306.1; -.
MGD; MGI:95550; Flt31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=94084791; PubMed=7505204;
Lyman S.D., James L., Vandenbos T., Devries P., Brasel K.,
Gliniak B., Hollingsworth L.T., Picha K.S., McKenna H.J.,
Splett R.R., Fletcher F.A., Maraskowy E., Farrah T.,
FOxworthe D., Williams D.E., Beckmann M.P.;
"Molecular cloning of a ligand for the flt3/flk-2 tyrosine kinase receptor: a proliferative factor for primitive hematopoietic cells.";
Cell 75:1157-1167(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hannum C., Culpepper J., Campbell D., McClanahan T., Zura Bazan J.F., Kastelein R., Hudak S., Wagner J., Mattson J. Duda G., Martina N., Peterson D., Menon S., Shanafelt A., Muench M., Kelner G., Namikawa R., Rennick D., Roncarolo Zlotnik A., Rosnet O., Dubreuil P., Birnbaum D., Lee F., "Ligand for FLT3/FLK2 receptor tyrosine kinase regulates haematopoietic stem cells and is encoded by variant RNAs. Nature 368:643-648(1994).
                                                                                                                                                                                                                                                                     use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entrepean Bioinformatics Institute. There are no restitute the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        McClanahan T., Culpepper J., Campbell D., Wagner J., Franz Bacon K., Mattson J., Tsai S., Luh J., Guimares M.J., Mattei M.-G., Rosnet O., Birnbaum D., Hannum C.; Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: STIMULATES THE PROLIFERATION OF EARLY HEMATOPOIETIC CELLS. SYNERGIZES WELL WITH A NUMBER OF OTHER COLONY STIMULATING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Identification of soluble and membrane-bound isoforms flt3 ligand generated by alternative splicing of mRNAs. Oncogene 10:149-157(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A., AND ALTERNATIVE MEDLINE=95124710; PubMed=7824267; Lyman S.D., James L., Escobar S., Do
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Structural analysis of human and murine flt3 ligand genomic loci."; Oncogene 11:1165-1172(1995).
                                                                                                                                                                                                                                       or send an
                                                                                                                                                                                                                                                         entities requires a license agreement
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                                                                                                                                                                                                                                                                                                                                                                                       FACTORS AND INTERLEUKINS.
SUBUNIT: Homodimer (soluble isoform) (By similarity).
SUBCELLULAR LOCATION: Type I membrane protein. Two so
isoforms are also produced by alternative splicing. (
isoform 3/E6, is biologically active, while the other
4/E6Deltal6, is inactive.
ALTERNATIVE PRODUCTS: 4 isoforms; 1/6C (shown here).
                                                                                                                                                                                                                                                                                                                                                              and 4/E6Delta16; are produced by alternative splicing
                                                                                                                                                                                                                                       email to license@isb-sib.ch).
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M.P., Copeland
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(See http://www.isb-sib.ch/announce/
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RESULT 3
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This SWISS-PROT entry is copyright. It is produced through a cobetween the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fcentities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIGNAL
                                                                                                    SEQUENCE FROM N.A.

MEDITINE-86306657; PubMed-3018124;

Davison A.J., Scott J.E.;

"The complete DNA sequence of varicella-zoster virus.";

J. Gen. Virol. 67:1759-1816(1986).

-!- FUNCTION: MODULATE ALPHA TRANS-INDUCING FACTOR-DEPENDENT
                                                                                                                                                                               Alphaherpesvirinae; NCBI_TaxID=10338;
                                                                                                                                                                                                  Varicella-zoster virus (strain Dumas)
Viruses; dsDNA viruses, no RNA stage;
                                                                                                                                                                                                                                01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
01-NOV-1990 (Rel. 16, Last annotation updat
Alpha trans-inducing factor 74 kDa protein.
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                                                                                            ACTIVATION OF ALPHA GENES.
                                                                                                                                                                                                                                                                                                                                                                                                                                     VASNLQDEELCGGLWRLVLAQRWMERLKTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MTVLAPAWSP-TTYLLLLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVT
                                                                                                                                                                                                                                                                                                                                          ELPEPRPRQLLLLLLLLLPLTLVLLAAAWGLRWQRARRR----GELHPGVPLP
                                                                                                                                                                                                                                                                                                                                                   APTAPQPP---LLLLLLEVGLLLLAAAWCLHWQRTRRRTPRPGEQVPPVPSP
                                                                                                                                                                                                                                                                                                                                                                                             LREVQTNISRLLQETSEQLVALKPWITR--QNFSRCLELQCQPDSSTLPPPWSPRPLEAT
                                                                                                                                                                                                                                                                                                                                                                                                                          VAVNLQDEKHCKALWSLFLAQRWIEQLKTVAGSKMQTLLEDVNTEIHFVTSCTFQPLPEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MTVLAPAWSPNSSLLLLLLLLSPCLRGTPDCYFSHSPISSNFKVKFRELTDHLLKDYPVT
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CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
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SL CYTOKIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ISOFORM 4).
A -> G (IN REF. 1).
MISSING (IN REF. 2).
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                                                                                                                                                                                                                                                                                      PRT;
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                                                                                                                                                                                                                                 tion update)
a protein.
                                                                                                                                                                                                                                                                                      661
                   (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                   Herpesviridae;
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.6e-57;
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                                                              a collaboration
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ID GATE
AC 075899
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DT 651) GAMMA-
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GBR2_HUMAN STANDARD; PRT; 941 AA.
075899; 075874; 075975; Q9UNS9; Q9UNR1; Q9P1R2;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF03387; Herpes_UL46; 1
Transcription regulation; TransEQUENCE 661 AA; 74272 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-Brain;
MEDLINE-20193514; PubMed-10727622;
Clark J.A., Mezey E., Lam A.S., Bonner
"Distribution of the GABA(B) receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GABA(B) receptor.";
Nature 396:679-682(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. TISSUE=Cerebellum; MEDLINE=99087321; I
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PIR; C27342; TNBE12.
                                                            TISSUE-Hippocampus;
Borowsky B., Laz T.,
Submitted (JAN-1999)
                                                                                                                                                                                                                                               Herzog H.;
"Cloning and charac
with high affinity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              White J.H., Wise A., Main M.J., Green A., Fraser N.J., Barnes A.A., Emson P., Foord S.M., Marshall F.H.; "Heterodimerization is required for the formation of a GABA(B) receptor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, NCBL_TaxID=9606;
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                                                                                                                                                                                                                         Submitted
                                                                                                                                                                                                                                                                                                                                           Liu M.,
                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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      SEQUENCE
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                                                                                                                                                                                                                                                                                                                                           Parker R.,
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                                                                                                                                                                                                                                                                               and characterization of a novel human
      FROM
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                                                                                                                                                         (ISOFORM
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McCrea K.,
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26.68;
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MW; C5CA77A16D365379 CRC64
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                                                                                                                                                                                                                                                                                                                                                                        2A).
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                                                               C.;
EMBL/GenBank/DDBJ databases
                                                                                                                                                         2A)
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Pred. No.
                                                                                                                                                                                                                                                                                                                                               Watson
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                                                                                                                                                                                                                                                                                                                                           J.
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2.7;
                                                                                                                                                                                                                                                                                                                                           Baker
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                                                                                                                                                                                                                                                                                                                                           E.
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                                                                                                                                                                                                                                                     baclofen.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 G.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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J. Pharmacol. Exp. Ther. 293:460-467(2000).

-i. FUNCTION: RECEPTOR FOR GABA. THE ACTIVITY OF THIS RECEPTOR IS.

-I. FUNCTION: RECEPTOR FOR GABA. THE ACTIVITY OF THIS RECEPTOR IS.

-I. MEDIATED BY G.-PROTEINS THAT INHLBITS ADENYLYL CYCLASE ACTIVITY,

STIMULATES PHOSPHOLIPASE A2, ACTIVATES POTASSIUM CHANNELS,

INACTIVATES VOLTAGE-DEPENDENT CALCIUM-CHANNELS AND MODULATES

INOSITOL PHOSPHOLIPUS HYDROLYSIS. PLAYS A CRITICAL ROLE IN THE

FINE-TUNING OF INHIBITORY SYNAPTIC TRANSMISSION. PRE-SYNAPTIC

GABA-B-R INHIBIT NEUROTRANSMITER RELEASE BY DOWN REGULATING

GABA-B-R INHIBIT NEUROTRANSMITER RELEASE BY DOWN REGULATING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             receptor 4 supports the GABA(B) heterodimer as the functional receptor.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=20237752; PubMed=10773016; Sullivan R., Chateauneuf A., Coulombe N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [8]
R1A-R2 INTERACTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Identification of a GABAB receptor subunit, gb2, required for functional GABAB receptor activity.";
J. Biol. Chem. 274:7607-7610(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=99175124; Pul
Ng G.Y.K., Clark J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GABABR1
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Martin S.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   O'Neill G.P., Liu Q.; "Cloning of a novel G-protein-coupled receptor GPR 51 resembling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ng G.Y.N., .....
Chateauneuf A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Fetal brain;
MEDLINE=99189236; Pu
Ng G.Y.K., McDonald
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mezey E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mol.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                               CEREBRAL CORTEX, THALAMUS, HIPPOCAMPUS, FRONTAL, OCCIPITAL AND TEMPORAL LOBE, OCCIPITAL POLE AND CEREBELLUM, FOLLOWED BY CORRUS CALLOSUM, CAUDATE NUCLEUS, SPINAL CORD, AMYGDALA AND MEDULLA WEAKLY EXPRESSED IN HEART, TESTIS AND SKELETAL MUSCLE.

DOMAIN: ALPHA-HELICAL PARTS OF THE C-TERMINAL INTERCELLULAR REGION MEDIATE HETERODIMERIC INTERRACTION WITH GABA-B RECEPTOR 1.

SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                       ALTERNATIVE PRODUCTS: 3 ISOFORMS; 2A (SHOWN HE PRODUCED BY ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: HIGHLY EXPRESSED IN BRAIN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MCCOEXPRESSION OF GABA-B-R1 AND GABA-B-R2 APPEARS TO PREREQUISITE FOR MATURATION AND TRANSPORT OF GABA-F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HIGH-VOLTAGE ACTIVATED CALCIUM CHANNELS, WHEREAS POSTSYNAPTIC GABA-B-R DECREASE NEURONAL EXCITABILITY BY ACTIVATING A PROMINENT INWARDLY RECTIFYING POTASSIUM (KIR) CONDUCTANCE THAT UNDERLIES THI LATE INHIBITORY POSTSYNAPTIC POTENTIALS. NOT ONLY IMPLICATED IN SYNAPTIC INHIBITION BUT ALSO IN HIPPOCAMPAL LONG-TERM SYNAPTIC INHIBITION SUCCESSION, SLOW WAVE SLEEP, MUSCLE RELAXATION AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBUNIT: HETERODIMER IS EFFECTIVE ON ITS C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANTINOCICEPTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PLASMA MEMBRANE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   56:288-295(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              expressed predominantly in nervous tissues and mapped
to the hereditary sensory neuropathy type 1 locus on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
RECEPTOR SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Neurosci. 13:180-191(1999).
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ld T., Bonnert T., Rigby M.,
Oulombe N., Kargman S., Cask
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HOMODIMERIC ASSEMBLY
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key T., Ev
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DOES NOT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sullivan R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TON
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                      VARIANT
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170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AJ012188; CAA09942.1;
AF056085; AAC63228.1;
AF095724; AAC63383.1;
AF095724; AAC63384.1;
AF095784; AAD30389.1;
AF074483; AAD03336.1;
AF074483; AAD03336.1;
AF0769755; AAC9345.1;
AF099033; AAD45867.1;
SPRPLEATAPTAPQPP----LLLLLLLPVGLLLLAAAWCLHWQRTRRRTPRPGEQVPPV
                                                                                                                                                                                                                                                                                                                                                                                                            PF01094; ANF_receptor; 1.
TE; PS00999; G_PROTEIN_RECEP_F3_1;
TE; PS00990; G_PROTEIN_RECEP_F3_2;
TE; PS00981; G_PROTEIN_RECEP_F3_3;
TE; PS0059; G_PROTEIN_RECEP_F3_4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AF074483; AAD03336.1;
AF069755; AAC99345.1;
AF099033; AAD45867.1;
                  Similarity 26; Conser
                                                                                                                                                                                                                                                                                                                                                                                                       coupled receptor;
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0003; 7tm_3; 1.
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                                                      941 AA;
                   Conservative
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44.1%;
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                                                     /FTId=VAR_010149.

S -> R (IN REF. 5).
P -> R (IN REF. 5).
G -> E (IN REF. 3).
MW; 09F1773DB0673C5D C
                  2;
                                                                                                                                                                                                                                                                                                                                                                                             Transmembrane; Glycoprotein; ed coil; Alternative splicing
                           Score
Pred.
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T -> A
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                                                                                                                         WPLRTTRMALRWTGRGRGRLGT Y -> F.
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V (POTENTIAL)
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                                                                                                                                                                                        N-LINKED
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                                                                                                                                                                                                                                                                                                                      II (POTENTIAL)
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                   Mismatches
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                   Indels
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(POTENTIAL).
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                                      941;
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                   9;
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CARBOHYD
                                                                                                                                                                                    TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sakamoto A., Ono K., Abe M., Jasmin G., Eki T., Murakami Y., Masaki T., Toyo-oka T., Hanaoka F.; Masaki T., Toyo-oka T., Hanaoka F.; Both hypertrophic and dilated cardiomyopathies are caused by mutation of the same gene, delta-sarcoglycan, in hamster: an animal model of disrupted dystrophin-associated glycoprotein complex."; proc. Natl. Acad. Sci. U.S.A. 94:13873-13878(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Alpha-sarcoglycan precursor (Alpha-SG) (Adhalin)
associated glycoprotein) (50DAG).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-98054328; PubMed-000
Sakamoto A
                                                                                                                                                                                                                                                                                            entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                      the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEBS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-F1B; TISSUE-Skeletal muscle;
MEDLINE-95278335; PubMed-7758576;
                                                                                                                                   SEQUENCE
                                                                                                                                                                         DOMAIN
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EMBL; U21677;
                                                                                                                                                                                                                                                                                                                                                             between
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SGCA_MESAU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Adhalin mRNA and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-OCT-2001
                                     115
                                                            11
              71
                                                                                                Local
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1 Lett.";

1 Lett. 364:245-249(1995).

FUNCTION: COMPONENT OF THE SARCOGLYCAN COMPLEX, A FUNCTION: COMPONENT OF THE SARCOGLYCAN COMPLEX, A FUNCTION: COMPONENT OF THE STRACELLULAR MATRIX.
                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE SPECIFICITY: STRONGLY
                                                                                                                                                                                                                                                                                                                                                                                                             HEART MUSCLE
                                                                                                                                                                                                                                                                                                                                                                                                                                      (Potential)
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            GGLWRL----
                                  TTRQRLLLLI-----EDPEGPRLPYQAEFLVRSHDVEEVL----PSTPANRFL--TAL
                                                         TTYLLLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASNLQDEELC
                                                                                                Similarity
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                                                                                   Conservative
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                                                                                                                                                                                                                                                            BAA12025.1; -.
AAA81645.1; -.
                                                                                                                                                                                                                                                Transmembrane;
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            ·---VLAQRWMERLKTVAGSKMQGLLERVNTEIHFVT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SSUE-Heart muscle;
PubMed=9391120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cDNA sequence are
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387
290
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335
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Chordata; Craniata; Vertebrata; E
Rodentia; Sciurognathi; Muridae;
                                                                                                                                   43326
                                                                                                23.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
                                                                                                                                                                                                                                                                                                                                                                                                TO THE SARCOGLYCAN ALPHA/EPSILON FAMILY.
                                                                                                                                    ₹:
                                                                                               Score 89;
Pred. No.
                                                                                                                                              N-LINKED
                                                                                                                                                                                                                      Glycoprotein; Sign POTENTIAL. ALPHA-SARCOGLYCAN
                                                                                  Pred. No. 2.6;
Mismatches
                                                                                                                                                                       CYS-RICH
                                                                                                                                                                                  CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                               EXTRACELLULAR POTENTIAL.
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2.6;
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           В
RA Dunham I., Hunt A.R., Collins J.E., Bruskiewich R., Beare D.M.,
RA Clamp M., Smink L.J., Ainscough R., Almeida J.P., Babbage A.K.,
RA Bagguley C., Bailey J., Barlow K.F., Bates K.N., Beasley O.P.,
RA Bagguley C., Bailey J., Barlow K.F., Bates K.N., Beasley O.P.,
RA Bird C.P., Blakey S.E., Bridgeman A.M., Buck D., Burgess J.,
RA Burrill W.D., Burton J., Carder C., Carter N.P., Chen Y., Clark G.,
RA Cleeg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R.,
Cleeg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R.,
RA Conroy D., Corby N.R., Coville G.J., Cox A.V., Davis J., Dawson E.,
RA Conroy D., Corby N.R., Coville G.J., Cox A.V., Davis J., Dawson E.,
RA Conroy D., Corby N.R., Fleming K., French L., Garner A.M.,
RA Gilbert J.G.R., Goward M.E., Grafham D.V., Griffiths M.N.D., Hall C.,
RA Hall R.E., Hall-Tamlyn G., Heathcott R.W., Ho S., Holmes S.,
RA Hall R.E., Jones M.C., Kershaw J., Kimberley A.M., King A.,
RA Laird G.K., Langford C.F., Leversha M.A., Lloyd C., Lloyd D.M.,
RA Martyn I.D., Mashreghi-Mohammadi M., Watthews L.H., Mccann O.T.,
RA McClay J., Mclaren S., McMurray A.A., Milne S.A., Mortimore B.J.,
RA Mclay J., Mclaren S., McMurray A.A., Milne S.A., Mortimore B.J.,
RA Waudin M., Walli M., Wallis J.M., Watthews L.H., Mccann O.T.,
RA Waudin M., Walli M., Walliamson H., Ramsey Y., Rogers L., Ross M.T.,
RA Waudin M., Walliams S.A., Williamson H., Wilmer T.E., Wilming L.,
RA Williams L., Hubbard T., Bentley D.R., Beck S., Rogers J., Shimizu N.,
RA Roe B.A., Chen F., Chu L., Crabtree J., Deschamps S., Do A., Do T.,
RA Roe B.A., Chen F., Chu L., Crabtree J., Deschamps S., Do A., Do T.,
RA Wang Q., Wang Y., Wang Z., White J., Willingham D., Wu H., Yao Z.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S3A1_HUMAN
Q15459;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kraemer A., Mulhauser F., Wersig C., Groning F "Mammalian splicing factor SF3al20 represents SURP family of proteins and is homologous to t factor PRP21p of Saccharomyces cerevisiae."; RNA 1:260-272(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   _HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   114) (SF3a120).
SF3A1 OR SAP114
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01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. MEDLINE=20057165; PubMed=10591208;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE-96079958; PubMed-7489498;
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. 35, Last sequence upd
. 41, Last annotation v
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i; Hominidae; Homo.
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a new member
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                                                             н. І.,
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Query Match
Best Local S
Matches 67
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T "Functional association of UZ snrnp with the ATP-independent plucesosmal complex E.";

T spliceosomal complex E.";

L Mol. Cell 5:779-787(2000).

C -!- FUNCTION: SUBBNIT OF THE SPLICING FACTOR SF3A REQUIRED FOR 'A'

C COMPLEX ASSEMBLY FORMED BY THE STABLE BINDING OF UZ SNRNP TO THE BRANCHPOINT SEQUENCE (BPS) IN PRE-MRNA. SEQUENCE INDEPENDENT BINDING GF SF3A/SF3B COMPLEX UPSTREAM OF THE BRANCH SITE IS C ESSENTIAL, IT MAY ANCHOR UZ SNRNP TO THE PRE-MRNA. MAY ALSO BE INVOLVED IN THE ASSEMBLY OF THE 'E' COMPLEX.

C -!- SUBUNIT: COMPONENT OF SPLICING FACTOR SF3A WHICH IS COMPOSED OF ASSOCIATES WITH THE SPLICING FACTOR SF3A AND A 12S RNA UNIT TO FORM THE UZ SNALL NUCLEAR RIBONUCLEOPROTEINS COMPLEX (UZ SNRNP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zhan M., Zhang G., Chissoe S., Murray J., Miller N., Minx P., Fulton R., Johnson D., Bemis G., Bentley D., Bradshaw H., Bourne S., Cordes M., Du Z., Fulton L., Goela D., Graves T., Hawkins J., Hinds K., Kemp K., Latreille P., Layman D., Ozersky P., Rohlfing T., Scheet P., Walker C., Wamsley A., Wohldmann P., Pepin K., Nelson J., Korf I., Bedell J.A., Hillier L., Mardis E., Waterston R., Wilson R., Emanuel B.S., Shaikh T., Kurahashi H., Saitta S., Budarf M.L., McDermid H.E., Johnson A., Wong A.C.C., Morrow B.E., Edelmann L., Kim U.J., Shizuya H., Simon M.I., Dumanski J.P., Peyrard M., Kedra D. Seroussi E., Fransson I., Tapia I., Bruder C.E., O'Brien K.P., Wilkinson P., Bodenteich A., Hartman K., Hu X., Khan A.S., Lane L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                        modified and this statement (See his entities requires a license agreement (See his or send an email to license@isb-sib.ch).
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use by non-profit institutions as 10
modified and this statement is not remo
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Tilahun Y., Wright H.;
                                                                                                                                     DOMAIN
                                                                                                                                                                                                       REPEAT
                                                                                                                                                                                                                        REPEAT
                                                                                                                                                                                                                                                      PROSITE;
                                                                                                                                                                                                                                                                                                                      InterPro; IPR000061;
InterPro; IPR000626;
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TISSUE SPECIFICITY: UBIQUITOUSLY EXPRESSED.
SIMILARITY: CONTAINS 1 UBIQUITIN-LIKE DOMAIN.
SIMILARITY: TO YEAST PRE-MRNA SPLICING FACTOR PRP21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SWISS-PROT entry is copyright. It is produced through a collaboration even the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way fied and this statement is not removed. Usage by and for commercial
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AC004997; AAC2.
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; SM00213; UBQ;
TE; PS50053; UB:
                                                                                                                                                                                                                                                                                                     PF00240; ubiquitin;
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 67;
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                   Similarity
   Conservative
                                                                                                                                                                                                                                      mRNA
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                                                                                                                                                                                                                                      processing;
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208
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560
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22.3%;
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                                                                   MW;
Score 89; DB Pred. No. 5.8; 34; Mismatches
                                                                                                 POLY-PRO.
POLY-GLU.
POLY-GLU.
POLY-PRO.
POLY-PRO.
                                                                 POLY-PRO.
7259F1EC4577305C CRC64;
                                                                                                                                                                                                    ; mRNA splicing; SURP MOTIF 1. SURP MOTIF 2.
                                                                                                                                                                                    UBIQUITIN-LIKE.
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(See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                          Nuclear protein;
 79;
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 120;
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4 LAPAWSPTTYLLLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASN 63

HSSP;

MGD; MGI:104875;

Ltbr

IPR001368;

TNFR_c6

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RESULT 7
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                                                                                                                                                                                                                                           sequence trap and chromosomal mapping., sequence trap and chromosomal mapping., Genomics 30:312-319(1995).

-i- FUNCTION: Receptor for the heterotrimeric lymphotoxin containing TRAF3 and LTB, and for TNPS14/LIGHT. Promotes apoptosis via TRAF3 LTA and LTB, and for TNPS14/LIGHT.
                                   EMBL;
EMBL;
                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                            and
                                                                                                                 use by non-profit institutions as long modified and this statement is not removed
                                                                                                                                                                                                                                                                                                                                                                                                                    Browning J.L., Ware C.F.;
Mouse lymphotoxin-beta receptor. Molecular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                          or send
                                                                                                       entities
                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. MEDLINE=96163885;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=96072804; PubMed=7594541;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tumor necrosis factor receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-1996 (Rel. 34, 01-OCT-1996 (Rel. 34, 15-JUN-2002 (Rel. 41,
                                                                                                                                                                                                                                                                                                    "The murine lymphotoxin-beta receptor cDNA: isolation sequence trap and chromosomal mapping.";
                                                                                                                                                                                                                                                                                                                              Honjo T
                                                                                                                                                                                                                                                                                                                                          Nakamura T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                  Force W.R., Walter B.N., Hession Browning J.L., Ware C.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Lymphotoxin-beta receptor). LTBR OR TNFRSF3 OR TNFCR.
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01-0CT-1996
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                                                                                                                                                                                                                                                                                                                                                                                              Immuno1.
                                                                                                                                                                                       (By similarity).
SUBUNIT: Self-associates (By similarity)
SUBCELLULAR LOCATION: Type I membrane pro
SUBCELLULAR IOCATIONS 4 TNFR-CYS REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                            expression."
                       U29173; AAA68964.1;
L38423; AAB00846.1;
U30798; AAA81334.1;
O14763; IDOG.
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Self-associates (By UNIT: Self-associates (By
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                                                                                        email to license@isb-sib.ch).
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Rodentia;
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Last annotation update)
receptor superfamily member 3 precursor
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01-FEB-1991 (Rel. 17, C
16-OCT-2001 (Rel. 40, L
15-JUN-2002 (Rel. 41, L
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                                   SEQUENCE FROM N.A.
MEDLINE=91006056; PubMed=2120044;
Jimenez J., Alphey L., Nurse P.,
                                                                                           Ce11
[2]
                                                                                                             SEQUENCE FROM N.A.

MEDLINE-89195217; PubMed=2702688;
Edgar B.A., O'Farrell P.H.;

"Genetic control of cell division
Cell 57:177-187(1989).
                                                                                                                                                                                                                          Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REPEAT
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                   "Complementation
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hatase (EC 3.1.3.48) (String protein) (Cdc25-like
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A de Pablos B. Delcher A. Deng Z. Mays A.D. Dew I. Dietz S.M.,

A de Pablos B. Delcher A. Deng Z. Mays A.D. Dew I. Dietz S.M.,

A Dodson K. Doup L.E. Downes M. Dugan-Rocha S. Dunkov B.C. Dunn P.,

A Durbin K.J. Evangelista C.C., Ferriaz C., Felschmann W.,

A Bourbin K.J. Evangelista C.C., Ferriaz C., Felschmann W.,

A Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,

RA Hostin D., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,

RA Ralbort K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,

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RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,

RA Svirskas R., Tector C., Turner R., Venter E., Mang A.H., Wang X.,

RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,

RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,

RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,

RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O.,

RA Zheng X.H., Zhong F.N., Rubin G.M., Venter J.C.,

RA Zheng X.H., Zhong F.N., Rubin G.M., Venter J.C.,

RA Zheng X.H., Zhong F.N., Rubin G.M., Venter J.C.,

RA Zibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,

RA Zibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,

RA Sibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,

"The genome sequence of Drosophila melanogaster.";

Science 287:2185-2195(2000)

C. -i- FUNCTION: THIS PROTEIN FUNCTIONS AS A DOSAGE-DEPENDENT INDUCER IN

MITOTIC CONTROL. IT IS A TYROSINE PROTEIN HOSPHATASE REQUIRED FOR

MITOTIC CONTROL. IT IS A TYROSINE PROTEIN PHOSPHATASE REQUIRED FOR

PRACE 287:2185-2195(2000)

C. -i- CATALYTIC ACTIVATE THE 294(CDC2) KINASE ACTIVITY.

C. -- CATALYTIC ACTIVATE THE POTCEIN TYROSINE PROSPHATE H H(2)0 - protein
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                                                                                                                                                                                                                EMBL;
                                                                                                                                                                                                                                                                                                           entities requires a or send an email to
                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restues by non-profit institutions as long as its content
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                                                                                                                                                                                                                   EMBL; M24909; AAA28916.1; -. EMBL; X57495; CAA40732.1; -. EMBL; AE003768; AAF56885.1;
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Amanatides P.G., Schere
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string.";
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SIMILARITY: BELONGS TO THE MPI PHOSPHATASE
SIMILARITY: CONTAINS 1 RHODANESE DOMAIN.
                                                                                                                                                              A32290; A32290.
S12008; S12008.
                                                                                                                                                                                                                                                                                                                                  an email to license@isb-sib.ch).
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Celniker S.E., Holt R.A., Evans C.A., Gocayn, Celniker S.E., Lit P.W., Hoskins R.A., Gass P.G., Scherer S.E., Li P.W., Ashburner M., Hend G., Wortman J.R., Yandell M.D., Zhang Q., Chen R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pf. Doyle C., Baxter E.G., Helt G., Nelson C.R., M.
                                                                                                                                                                                                                                                                                                                                                             agreement
                                                                                                                                                                                                                                                                                                                                                                                       is not removed.
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Welson C.R., Miklos G.L.G.
                                                                                                                                                                                                                                                                                                                                                                                             Usage
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Baldwin D.,
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HSSP; P30304; 1C25. FlyBase; FB9n0003525; stg. InterPro; IPR000751; MPI_Phosphatase. InterPro; IPR001763; Rhodanese-like. Pfam; PF00581; Rhodanese: 1.

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Q63474;
Q1-NOV-1997
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CONFLICT
SEQUENCE
 between
the Euro
                                                                                                                                                               STRAIN=Sprague-Dawley; TISSUE-Brain;
MEDLINE=94173920; PubMed=8127887;
Sanchez M.P., Tapley P., Saini S.S., He B., Pulido D., Barbacid
"Multiple tyrosine protein kinases in rat hippocampal neurons:
isolation of Ptk-3, a receptor expressed in proliferative zones
the developing brain.";
Proc. Natl. Acad. Sci. U.S.A. 91:1819-1823(1994).
-i- FUNCTION: MAY BE INVOLVED IN CELL-CELL INTERACTIONS AND
RECOGNITION (BY SIMILARITY).
-i- CAPALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
tyrosine phosphere
                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Epithelial discoidin domain receptor 1 precursor (EC 2.7.1.112)
(Tyrosine-protein kinase CAK) (Cell adhesion kinase) (Tyrosine kinase
                            This
                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10116;
[1]
                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
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                                                               SIMILARITY: CONTAINS SIMILARITY: BELONGS
                                                                                                    TISSUE SPECIFICITY:
PROLIFERATIVE ZONES
SIMILARITY: WITH THE
 European
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   division; Mitosis; Hydrolase.

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ENCE 479 AA; 54094 MW; 684
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MTVLAPAWSPTTYLLL----LLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LEATAPTA----POPPLILLLLLPVGLLLLAAAWCLHWQRTRRTPRPGEQVPPVPSFQDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CSMESSMDDE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VTVASNIQDEELCGGLWRLVLAQRWMERLKTVAGSKMQGLLERVNTEIHFVTKCAFQPPP :: |:: |: | : | : |
                                                                                                                                                                                                                                                                                                                                                                                                       (Discoidin receptor tyrosine kinase) (Protein-tyrosine kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LLVEH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SCLRFVQTNISRLLQETSEQLVALKP---WITRQNFSRCLEL-QCQPDSSTLPPPWSPRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---TARDCFKRPEPP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SGLN----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
56; Conserv
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                                                 SUBFAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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22.9%;
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THE 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 4.4,
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 87.5; DF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BY SIMILARITY.
A -> T (IN REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RHODANESE
                                                                                                                  E DEVELOPING
                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Rat
                                                               '8 TYPE C DOM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -ASANCSPIQSKRHRCAAVEKENCPAPSPLSQ
                                                                                                   embrane protein.

BRYONIC AND ADULT TISSUES; ALSO
ELOPING BRAIN; HIPPOCAMPAL NEURONS
CATALYTIC DOMAINS OF TYR-PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               910
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                                                                KINASES.
                                                                                                                                                                                                                                                             Barbacid
                                                                                                                                                                     protein
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                                                                                                                  ALSO
NEURONS
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Best Local S
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CARBOHYD
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CARBOHYD
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BINDING
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DOMAIN
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DOMAIN
DDRI_MOUSE STANDARD; PRT; 911 AA. Q03146; 01-OCT-1994 (Rel. 30, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Epithelial discoidin domain receptor 1 precurs (Tyrosine-protein kinase CAK) (Cell adhesion )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00069; pkinase; 1.

Pfam; PF00754; F5_F8_type_C; 1.

Pfam; PF0070001; Euk_pkinase; 1.

SMART; SM000231; F558C; 1.

SMART; SM000219; TyrKC; 1.

PROSITE; PS00109; PROTEIN_KINASE_TYR; 1

PROSITE; PS00139; RECEPTOR_TYR_KIN_II;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PROSITE;
                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; L26525; HSSP; P00523;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or send an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transterase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS50011; PROTEIN_KINASE_DOM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro;
                                                                                                                471
                                                                                                                                    215
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                                                                                                                                                                                                356
                                                                                                                                                                                                                    143
                                                                                                                 NRPGPREPPPYQEPRPRGTPTHSAPCVPNGSALLL
                                                                                                                                    PRPGEQVPP----
                                                                                                                                                                                                PWLLESEISFISDV-VNDSSDTFPPAPWWPPGPPPTNFSSLELEPRGQQPVAKAEGSPTA
                                                                                                                                                                                                                   PWITRONESRCLELQCOPDSSTLPP-PW---SPRPLEATA---
                                                                                                                                                         ILIGCLVAIILLLLIIALML---
                                                                                                                                                                                                                                        Similarity 24.5
38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PS01285;
PS01286;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IPR000719; Euk_pkinase.
IPR000421; FA58_C.
IPR002011; RTKinaseII.
IPR001245; Tyr_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              equires a license agreement (See http://www.isb-sib.ch/announce/email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                  910
                                                                                                                                                                     PLLLLLLPVGLLLLAAAWCLHWQR----TRRR---
                                                                                                                                                                                                                                                                                                     378
473
607
613
652
763
763
7793
7793
7794
212
261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tyrosine-protein kinase; Glycion; Transmembrane; Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAA21089.1;
                                                                                                                                                                                                                                                                               AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; FA58C_1; FA58C_2;
                                                                                                                                                                                                                                                                                          412
598
902
621
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763
186
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2212
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910
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                                                                                                                                                                                                                                                                                  101164
                                                                                                                                                                                                                                                 7.0%;
                                                                                                                                                                                                                                         12;
                                                                                                                                                                                                                                                                                  MW.
                                                                                                                                                                                                                                                                              PHOSPHORYLATION (AUTO
PHOSPHORYLATION (AUTO
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PHOSPHORYLATION (AUTO
N-LINKED (GLCNAC...
N-LINKED (GLCNAC...
N-LINKED (GLCNAC...
N-LINKED (GLCNAC...
                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL).

GLY/PRO-RICH.

GLY/PRO-RICH.

GLY/PRO-RICH.

PROTEIN KINASE.

ATP (BY SIMILARITY).

ATP (BY SIMILARITY).

BY SIMILARITY.

BY SIMILARITY.
                                                                                                                                                                                                                                        Score 87; DB
Pred. No. 10;
L2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
CYTOPLASMIC
F5/8 TYPE C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EPITHELIAL DISCOIDIN DOMAIN EXTRACELLULAR (POTENTIAL).
                                                                                                                                                         -WRLHWRRLLSKAERRVLEEELTVHLSVPGDTILIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.
                                                                                                                                   VPSPQDLLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Glycoprotein; Stor; ATP-binding
           precursor (EC
                                                                                                                 505
                                                                                                                                    232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          (PHOSPHOLIPID-BINDING
                                                                                                                                                                                                                                                            1;
                                                                                                                                                                                                                                                                                                                                          (AUTO-)
   kinase)
                                                                                                                                                                                                                                         35;
                                                                                                                                                                                                                                                                                                                                 (AUTO-)
                                                                                                                                                                                                                                                           Length
                                                                                                                                                                                                                    PTAPQP-----
                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                      -) (BY SIMILARITY).
-) (BY SIMILARITY).
-) (BY SIMILARITY).
-) (BY SIMILARITY).
) (DOTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Signal;
                                                                                                                                                                                                                                                                                          (POTENTIAL)
                                                                                                                                                                                                                                                                                                             (POTENTIAL).
                                                                                                                                                                                                                                                                                                      (POTENTIAL)
  (Tyrosine
           2.7.1.112)
                                                                                                                                                                                                                                                             910;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RECEPTOR
                                                                                                                                                                                                                                         70;
                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                 414
                                                                                                                                                                                                                    184
                                                                                                                                                                             214
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DDR) (Discoidin

receptor

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SMART; SM00231; FA58C; 1.

SMART; SM00219; TyrKG; 1.

SMART; SM00219; TyrKG; 1.

PROSITE: PS00107; PROTEIN_KINASE_ATP; FAI

PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.

PROSITE: PS00239; RECEPTOR_TYR_KIN_II; 1.

PROSITE: PS01285; FA58C_1; 1.

PROSITE: PS01286; FA58C_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                          HSSP; P00523; 2PTK.
MGD; MGI:99216; Ddr1.
InterPro; IPR000719; E
InterPro; IPR000421; E
                                 SIGNAL
CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oncogene 7:2499-2506(1992).
-!- FUNCTION: MAY BE INVOLVED IN CELL-CELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chestier A., Wilkinson D.G., Charnay P.;
"An Eph-related receptor protein tyrosine k:
expressed in the developing mouse hindbrain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 766-822 FROM N.A. STRAIN-C57BL/6; TISSUE-Embryonic MEDLINE-93096484; PubMed-1281307;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=96204002; PubMed=8622863; Perez J.L., Jing S.Q., Wong T.W.; Perez J.L., Jing S.Q., Wong T.W.; Identification of two isoforms of the Cak receptor kinase that are coexpressed in breast tumor cell lines."; Oncogene 12:1469-1477(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DDR1 OR EDDR1 OR CAK OR MPK6.
Mus musculus (Mouse).
Eukaryota, Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; L57509; AAB05209.1;
EMBL; X57240; CAA40516.1;
PIR; S30502; S30502.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gilardi-Hebenstreit P., Nieto M.A., Frain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-C57BL/6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                         Alternative
                                                                                             Transferase; Tyrosine-protein Phosphorylation; Transmembrane
                                                                                                                                                                                                                                                                                                                                   Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 <u>.</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ÷
                                                                                                                                                                                                                                                                                                                                                                             InterPro;
                                                                                                                                                                                                                                                                                                                                                                                               InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPOSINE Phosphate.

1. SUBCELLULAR LOCATION: Type I membrane protein.

1. ALTERNATIVE PRODUCTS: 2 ISOFORMS; CAK I (SHOWN I ARE PRODUCED BY ALTERNATIVE SPLICING. THEY ONLY ABSENCE OF A 37 RESIDUES SEGMENT.

1. TISSUE SPECIFICITY: THE PREDOMINANT ISOFORM CAK DEVELOPING EMBRYO AND ADULT BRAIN; CAK II IS EXECUTED THE LIAL CELLS.

1. SUBLIARITY: BELONGS TO THE TYR FAMILY OF PROTEING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         send an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Buropean Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way iffed and this statement is not removed. Usage by and for commercial ities requires a license agreement (See http://www.isb-sib.ch/announce/send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RECEPTOR SUBFAMILY.
SIMILARITY: CONTAINS 1 F5/8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CATALYTIC ACTIVITY: ATP + a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RECOGNITION (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EM
                                                                                                                                                                                                                                                                                                    PF00069; pkinase; 1.
    PF00754; F5_F8_type_C; 1.
    PD000001; Euk_pkinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FROM N.A., AND ALTERNATIVE
                                                                                                                                                                                                                                                                                                                                                                    IPR000719; Euk_pkinase.
IPR000421; FA58_C.
IPR002011; RTKinaseII.
IPR001245; Tyr_pkinase.
'Y'.
Lion' Tr.
'e splicing.
19
1 19
1911
414
                                                                                             Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tyrosine
        POTENTIAL.
EPITHELIAL DISCOIDIN
EXTRACELLULAR (POTENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata; | Sciurognathi; Muridae;
                                                                                                                kinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE
                                                                                          Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                kinase) (Protein-tyrosine kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPLICING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           O.
                                                                                      Glycoprotein; Si
tor; ATP-binding;
                                                                                                                                                                                                                                          FALSE_NEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tyrosine -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        THEY ONLY
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             (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ONLY
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S EXPRESSED
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                            DOMAIN
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Y DIFFER B
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; Murinae; Mus
                                                                                                              Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             +
                               RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL
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RESULT
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                                                                                                                                                                                                          Bos taurus (Bovine).
Eukaryota; Metazoa; (
Mammalia; Eutheria; (
Bovidae; Bovinae; Bos
                                                                                                                                                                                                                                                          CNG4_BOVIN STANDARD; PRT; 1394 AA.

Q28181; Q28082; Q03861;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
240 kDa protein of rod photoreceptor CNG-channel [Contains: Glutamic acid-rich protein (GARP); Cyclic-nucleotide-gated cation channel 4 (CNG channel 4) (CNG-4) (Cyclic nucleotide-gated cation channel modulatory subunit)].
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MOD_RES
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VARSPLIC
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CARBOHYD
CARBOHYD
MEDLINE-96198098; PubMed-8626431;
Biel M., Zong X., Ludwig A., Sautter A.,
"Molecular cioning and expression of the
cyclic nucleotide-gated cation channel.";
J. Biol. Chem. 271:6349-6355(1996).
                                                                                                                                                                                                                                                                                                                                                                             LT 11
BOVIN
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DOMAIN
                                                                                                                                     SEQUENCE FROM N.A., AND PARTIAL SEQUENCE
MEDLINE-96009859; PubMed-7546742;
Koerschen H.G., Illing M., Selfert R., Se
Gotzes S., Colville C., Mueller F., Dose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                           "A 240 kDa protein represents nucleotide-gated channel from Neuron 15:627-636(1995).
                                                          TISSUE-Testis;
                                                                     SEQUENCE
                                                                                                                             Kaupp U.B., Molday R.S.;
                                                                                                                                                                                               NCBI_TaxID=9913;
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F5/8 TYPE C
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Dose A.,
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Godde M., Molday
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Best Local
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VARSPLIC
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TRANSMEM
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EMBL; X94707; CAA64367.1; -.
EMBL; M61185; AAAA3036.1; -.
InterPro; IPR000636; M+channel_nlg.
InterPro; IPR000595; CNMP_binding.
                                                                                                                                                                                                                                                                                                                                                                                                                     CHAIN
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PROSITE: PS00889; CNMP_BINDING_2; 1
PROSITE: PS50042; CNMP_BINDING_3; 1
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Pfam; PF00520; ion_trans; 1.
SMART; SM00100; cNMP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (S or send an email to license@isb-sib.ch).
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SEQUENCE OF 1-590
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115 PPPSCLRFVQTNISRLL---
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ALTERNATIVE PRODUCTS: 3 ISOFORMS; CNG4C (SHOWN HERE), CNG4D
AND CNG4E; ARE PRODUCED BY ALTERNATIVE SPLICING, CNG4D IS BY FAR
THE MOST FREQUENT FORM (CNG4D:CNG4E:CNG4E = 20:2:1) IN TESTIS.
TISSUE SPECIFICITY: RETINA, TESTIS, KIDNEY, HEART, AND BRAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ween the Swiss Institute of Bioinf
European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE SPECIFICITY: RETINA, TESTIS, KIDNEY, HEART, AND BRAIN. SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE-GATED CATION CHANNEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBUNIT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN
                               . Similarity
35; Conser
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1 590 GLUTAMIC ACID-RICH PROTEIN
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                               Conservative
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Pred. No. 18;
L3; Mismatches
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MISSING (IN ISOFORM CNG4E).
MISSING (IN ISOFORM CNG4D).
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EXTRACELLULAR (POTENTIAL)
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S. -> A (IN REF. 2).
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D -> E (IN REF. 2).
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RESULT 12
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RESULT 13
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P21997;
01-AUG-1991
01-AUG-1991
01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         J. Cell Biol. 109:3493-3501(1989)

-:- FUNCTION: THE EXTRACELLULAR MATRIX (ECM) OF VOLVOX CONTAINS
INSOLUBLE FIBROUS LAYERS THAT SURROUND INDIVIDUAL CELLS AT A
DISTANCE TO FORM CONTIGUOUS CELLULAR COMPARTMENTS. SSG 185 IS
MONOMERIC PRECURSOR OF THIS SUBSTRUCTURE (C3Z STRUCTURE). THE
COVALENT CROSS-LINKS ARE FORWED BETWEEN THE SACCHARIDE CHAINS
RATHER THAN BETWEEN THE POLYPEPTIDE CHAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Glycoprotein;
DOMAIN 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entitles requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales; Volvocaceae; Volvox.
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the cellular compartment.":
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 268
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                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PTM: A CENTRAL DOMAIN OF 77 AA CONSISTS ALMOST EXCLUSIVELY OF HYDROXYPROLINE RESIDUES.
                                                                                                                                                                                                QVPPVPSPQDLL
                                                                                                                                                PVPPPPSPPSVL
                                                                                                                                                                                                                                                PDSSTLPPPWSPRPLEATAPTAPQPPLLLLLLLPVGLLLLAAAWCLHWQRTRRRTPRPGE 219
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   X51616; CAA35953.1;
                                                                                                                                                                                                                                                                                                                                              l Similarity
21; Conser
  Q9UNQ3
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Nagariensis / HK10;
                                                                                                                                                                                                                                                                                                                                                                                                                                              260
485 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ESPSLPAPGPPEPEEPIP-EPQPTIQASSLPPPQDSARLMAWILH--RLEMAL
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                                                                                                                                                                                                                                                                                                                                                Conservative
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                      STANDARD;
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. 19, Last sequence update)
. 34, Last annotation updat
glycoprotein 185 (SSG 185)
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                                                                                                                                                                                                                                                                                                                                                                                                                                              50436 MW;
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                                                                                                                                                                                                                                                                                                                                                                       Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                            Score 86;
                         PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              A52216400A031421 CRC64;
                                                                                                                                                                                                                                                                                                                                              Mismatches
                         282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          485
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G 185).
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Best Local
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                                                                                                                                                                                                                                                                EMBL;
                                                                                                                                                                                                                                                                                                            between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                               of cyclic AMP-induced transcription for Mol. Cell. Biol. 19:5001-5013(1999).
                                                                                                                                                                                                                                                                                            entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
                                                                                                                                                           Transcription regulation; Multigene family.
                                                                                                                                                                   PROSITE; PS00036; BZIP_BASIC; 1.
Transcription regulation; DNA-binding; Activator;
                                                                                                                                                                                                                                           EMBL; AF101388; AAD28370.1; TRANSFAC; T04877; -.
                                                                                                                                                                                                                                                                           EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   factors
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Emson P.C.,
                                                                                                   SEQUENCE
                                                                                                            CONFLICT
                                                                                                                                DNA_BIND
                                                                                                                                          DOMAIN
                                                                                                                                                    DOMAIN
                                                                                                                                                                                                    InterPro; IPR004827; Pfam; PF00170; bZIP;
                                                                                                                                                                                                                         Genew; HGNC:790; ATF5.
MIM; 606398; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kohroki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "The GABAB receptor factors CREB2 and AT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE=20558615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID-9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATF5 OR ATFX.
                    66
                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION: THIS PROTEIN BINDS THE CAMP (CONSENSUS: 5'GTGACGT(A/C)(A/G)-3'), FUTRAL AND CELLULAR PROMOTERS.
                                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: Nuclear (By simil SIMILARITY: BELONGS TO THE BZIP FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                        SUBUNIT: BINDS DNA AS A DIMER (POTENTIAL). INTERACTS
                                     WIT-RONESRCLELQCOPDSSTLPPPWSPRP--LEATA----
 ---PTAPQPPLLLLLLPVGL---
                  WMTERVDFTALLPLEPPLPPGTLPQP-SPTPPDLEAMASLLKKELEQMEDFTLDAPPLPP
                                                                                                                                                                                                                                                               AF305687;
AB021663;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               E=99303793; PubMed=10373550;
., Meistrich M.L., Plon S.E.;
.Cdc34 and Rad6B ubiquitin-conjugating enzymes target repressors
                                                                                                                                                                                            SM00338;
                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OF 161-282 FROM N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ., Tanaka K
(DEC-1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Rel. 40, Createu)
(Rel. 40, Last sequence update)
(Rel. 41, Last annotation update)
dependent transcription factor ATF-5
ion factor 5) (Transcription factor AT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          58615; PubMed=11087824;
McIllhinney R.A.J., Wise A., Ciruela F., Cha
Billinton A., Marshall F.H.;
receptor interacts directly with the related
                                                                                                            123
186
210
236
161
                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and ATFx.";
cad. Sci. U.S.A.
                                                                                                                                                                                           BRLZ; 1.
                                                                                                                                                                                                                                                              AAG22558.1; -.
BAA78477.2; -.
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194
230
250
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                                                                   6.8%;
29.9%;
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                                                                                                  ME:
                                                          Score 85; DB Pred. No. 3.9; 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL/GenBank/DDBJ databases
                                                                                                          POLY-PRO.
BASIC MOTIF.
LEUCINE-ZIPPER (PROBABLE).
LLA -> RHE (IN REF. 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97:13967-13972(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata; Catarrhini; Hominidae.
                                                                                                 DDB2F907CA0215A0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                    similarity).
                                                                 DB
3.9;
LLLAAAWCLH - - WQRTRRRTPRPGEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                       proteolysis.";
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                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                           38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -5 (Activating ATFx).
                                                                            Length 282
                                                                                                                                                                    Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                      ELEMENT
                                                                                                                                                                                                                                                                                                                                                                                                                            PRESENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chan W.Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            transcription
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                                                          44;
                                                                                                                                                                                                                                                                                                                                                                                                         GABAB
                                                         Gaps
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                                      178
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RESULT 14
FCGN_RAT
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01-JAN-1990 (Rel. 4
15-JUN-2002 (Rel. 4
1GG receptor FCRN 1
receptor) (IGG FC 1
FCGRT OR FCRN.
                                                                                                                                                                                                                                                                                                                        Structure 6:63-73(1998).

Structure 6:63-73(1998).

-i- FUNCTION: BINNS TO THE FC REGION OF MONOMERIC IMMUNOGLOBULINS GAMMA. MEDIATES THE SELECTIVE UPTAKE OF IGG FROM MILK AND HELPS NEMBORN ANIMALS TO ACQUIRE PASSIVE IMMUNITY. IGG IN THE MILK IS BOUND AT THE APICAL SURFACE OF THE INTESTINAL EPITHELIUM. THE RESULTANT FCRN-IGG COMPLEXES ARE TRANSCYTOSED ACROSS THE INTESTINAL EPITHELIUM AND IGG IS RELEASED FROM FCRN INTO BLOOD C TISSUE FLUIDS (BY SIMILARITY).

-i- SUBUNIT: FCRN COMPLEX CONSIST OF TWO SUBUNITS: P51, AND P14 WHICE INTERPORTURE OF TWO SUBUNITS: P51, AND P14 WHICE OF THE SUBUNITY OF TWO SUBUNITS: P51, AND P14 WHICE OF 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Simister N.E., Mostov K.E.; "Cloning and expression of the neonatal rat intestinal Fc major histocompatibility complex class I antigen homolog." Cold Spring Harb. Symp. Quant. Biol. 54:571-580(1989).
                                                                                                                                      This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=95059482; PubMed=7969498;
Burmeister W.P., Huber A.H., Bjor
"Crystal structure of the complex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. TISSUE=Epithelium; MEDLINE=90315866;
                               use
                                                                   the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "An Fc receptor structurally related Nature 337:184-187(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Simister N.E., Mostov K.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-89097257;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-Wistar;
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Mammalia; Eutheria; Rodentia;
modified and this statement is not removed.
                                                                                                   between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-98154319; PubMed-
Vaughn D.E., Bjorkman P.J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  X-RAY CRYSTALLOGRAPHY (2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 372:379-383(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Crystal structure Fc.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Structural basis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            221
                                                                                                                                                                                                   TISSUE SPECIFICITY:
SIMILARITY: BELONGS
                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: Type TISSUE SPECIFICITY: INTESTI
                                                               European
                            SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                          LIKE HETERODIMER.
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                        the Swiss Institute of Bioinforma
pean Bioinformatics Institute. The
non-profit institutions as long
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13, Last sequence update)
41, Last annotation update)
4rge subunit P51 precursor (FCRN) (Neonatal large subunit receptor transporter, alpha chain).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APHY (2.2 ANGSTROMS).
PubMed=9493268;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PubMed=2534798;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PubMed=2911353;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Rat).
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                                                                                                                                                                                               N: Type I membrane protein.
INTESTINAL EPITHELIUM.
TO THE IMMUNOGLOBULIN SUPERFAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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ABF1_MOUSE
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Best Local S
Matches 51
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Pfam; PF00129; MHC_I; 1.
ProDom; PD000050; MHC_I; 1.
SMART; SM00407; IGcl; 1.
PROSITE; PS00290; IG_MHC; 1.
IgG-binding protein; Receptor
                                                                                                                                           ABF1_MOUSE
061329;
16-OCT-2001
16-OCT-2001
16-OCT-2001
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CARBOHYD
CARBOHYD
SEQUENCE
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DOMAIN
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CARBOHYD
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DOMAIN
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             SEQUENCE FROM N.A.
STRAIN-BALB/MK X ICR; TISSUE-Brain;
MEDLINE-96194902; PubMed-8654949;
Ido A., Miura Y., Watanabe M., Saka
                                                                                                             ATBF1
                                                                                                                     16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Alpha-fetoprotein enhancer binding protein (A
AT-binding transcription factor 1).
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PIR;
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Hashimoto
                                                                                       Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PDB; 1FRT; 14-FEB-95
PDB; 3FRU; 10-JUN-98
                                                                   NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR003006; Ig_MHC.
InterPro; IPR003597; Ig_c1.
InterPro; IPR001039; MHC_I.
                                                                               Mammalia;
                                                                                                                                                                                                                                           308
                                                                                                                                                                                                                                                                 196
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                                                                                                                                                                                                                                                                                                                                                                                            46
                                                                                                  musculus
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x; m35495;
s02117; s
A37374; A
                                                                                                                                                                                                                                           LLLVVVAIAGGVLLWNRMRSGLPAPWLSLSGDDSGDLLPGGNLPPEAEPQ 357
                                                                                                                                                                                                                                                                                    GDGSFHAWSLLEVKRGDEHHYQCQVEHEGLAQPLT---VDLDSPARSSVPVVGIIL---
                                                                                                                                                                                                                                                                                                LLLLA---AAWCLHWQRTRRRTPR-----PGEQVPPVPSPQ 228
                                                                                                                                                                                                                                                                                                                              ------TCAAFSFYPPELKFRFLRNGLA
                                                                                                                                                                                                                                                                                                                                                  NTEIHFVTKCA---FQPPPSCLRFVQTNISRLLQETSEQLVALKPWITRQNFSRC----
                                                                                                                                                                                                                                                                                                                                                                        RKESEFLLTSCP-----ERLLGHLERGRQNLEWKEPPSMRLKARPGNSGSSVL---
                                                                                                                                                                                                                                                                                                                                                                                            RELSDYLLQDYPVTVASNLQDEELCGGLWRLVLAQRWME-----RLKTVAGSKMQGLLERV 101
                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                             lus (Mouse).
; Metazoa; Chordata;
Eutheria; Rodentia;
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AAA41611.1;
     Morinaga T
                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Receptor; Transmembrane; Glycoprotein; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                          28;
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     M., Sakai
Nishi S.,
                                                                                                                                                                                                                                                                                                                                                                                                                 21;
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BY SIMILARITY.
N-LINKED (GLCN.
N-LINKED (GLCN.
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Pred.
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N-LINKED (GLCNAC. . .) (POTENTIAL);
8A8BF2873A698BB5 CRC64;
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CYTOPLASMIC (POTENTIAL).
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                                                                             Craniata; Ver
Sciurognathi;
                                                                                                                                                                                       PRT;
               Sakai M.,
                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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     Tamaok i
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                                                                             Vertebrata; Euteleostomi;
thi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1;
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     Inoue Y.,
aoki T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 366;
                                                                                                                                 motif-binding
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               Miki T.
                                                                                                                                                                                                                                                                                                                              SGSGNCSTGPN
                                                                                                                                                                                                                                                                                                                                                                                                                92;
                                                                                                                                  factor)
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                                                                                                                                                                                                                                                                                                                             253
                                                                                                                                                                                                                                                                                                                                                                                                                 11;
      TRANSFAC; T03881; ...

MGD: MGI:99948; Atbf1.

InterPro; IPR0001356; Homeobox.

InterPro; IPR00082; Znf_C2H2.

InterPro; IPR00082; Znf_U1.

Pfam; PF00046; homeobox; 4.

Pfam; PF00096; Zf-C2H2; 20.

ProDom; PD000010; Homeobox; 4.

SMART; SM00389; HOX; 4.

SMART; SM00389; HOX; 4.

SMART; SM00359; TMF_C2H2; 22.

SMART; SM00351; ZnF_U1; 7.

PROSITE; PS00027; HOMEOBOX_1; 2.

PROSITE; PS00028; ZINC_FINGER_C2H2_1; 15.

PROSITE; PS00028; ZINC_FINGER_C2H2_2; 2.

PROSITE; PS00028; ZINC_FINGER_C2H2_2; 2.
                                                                                                                                 ZN_FING
    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; D26046; BAA05046.1; -. HSSP; P20263; 10CP. TRANSFAC; T03881; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -:- FUNCTION: Transcriptional activator that sequence of the enhancer element of the -:- SUBCELULUAR LOCATION: Nuclear.
-:- SIMILARITY: CONTAINS 4 HOMEOBOX DOMAINS
                                                                                                                                                                                                                                                                                                                                                                                                                          Transcription regulation; Activator; DNA-binding; Homeobox; Nuclear protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Cloning of the cDNA encoding the mouse Gene 168:227-231(1996).
                                                                                                             DOMAIN
                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                    282
641
672
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     C2H2-TYPE

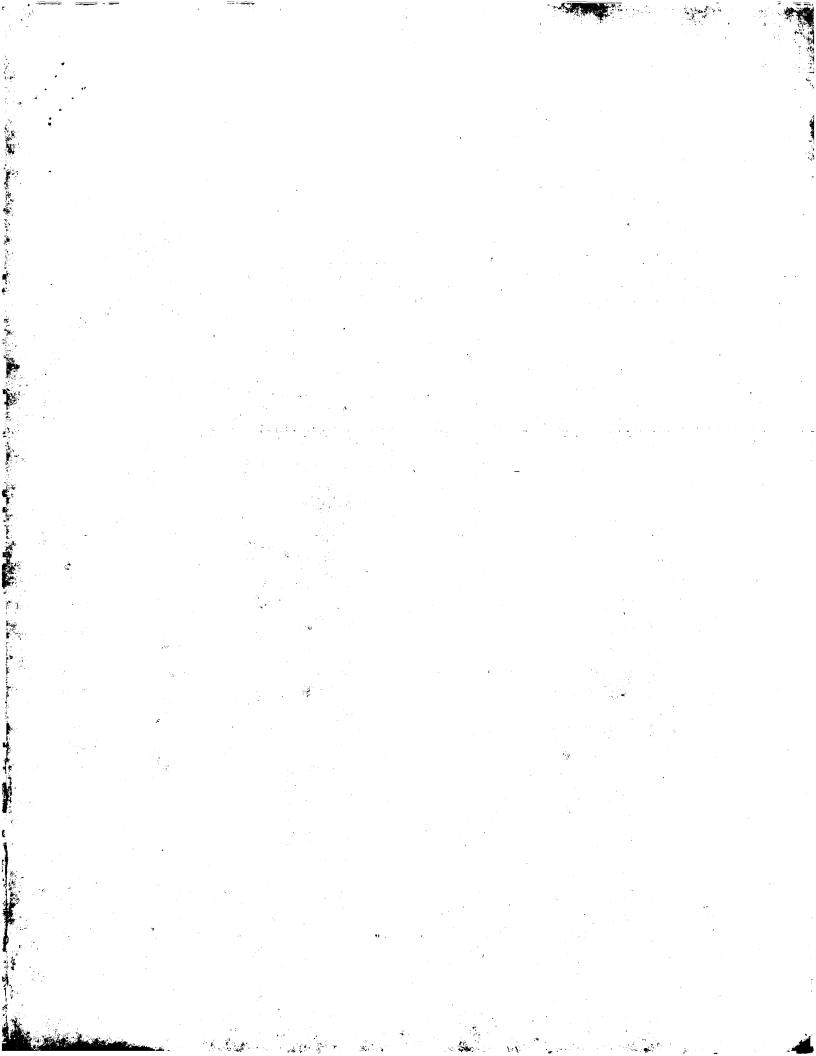
C2H2-TYPE
    POLY-GLN.
POLY-GLY.
                                                       POLY-GLN.
POLY-PRO.
                                                                                       C2H2-TYPE.
C2H2-TYPE.
POLY-GLU.
POLY-ALA.
POLY-ALA.
POLY-GLN.
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C2H2-TYPE.
C2H2-TYPE.
                                   POLY-ALA.
POLY-PRO.
                                                                                                                                                                                                                                                                                                                                                                                                                r protein;
C2H2-TYPE.
                                                                                                                                                        HOMEOBOX 4
                                                                                                                                                                 C2H2-TYPE
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E (DEGENERATE).
E (ATYPICAL).
E (ATYPICAL).
E (ATYPICAL).
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AFP gene.
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Search completed: May 27, 2003, 18:27:34 Job time : 15 secs	224 VPSPQ 228 : : 3225 IPAPQ 3229	171 PRPLEATAPTAPQPPLLLLLLLPVGLLLLAAAWCLHWQRTRRRTPRPGEQVPP 223	127 ISRLLQETSEQLVALKPWITRQNFSRCLELQCQPDSSTLPPPW	87 KTVAGSKMOGLLERVNTEIHEVTKCAFQPPPSCLREVQTN 126	29 DCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASNLQDEELCGGLWRLVLAQRWMERL 86	Query Match 6.8%; Score 84.5; DB 1; Length 3726; Best Local Similarity 21.6%; Pred. No. 80; Matches 53; Conservative 29; Mismatches 70; Indels 93; Gaps 12;	DOMAIN 3620 3623 POLY-PRO. DOMAIN 3659 3662 POLY-SER. SEQUENCE 3726 AA; 406567 MW; 915ACBE588A72C98 CRC64;



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Title:
Perfect score:
Sequence:
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Maximum
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Maximum Match 100%
Listing first 45 summaries
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1 MTVLAPAWSPTTY
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1: pir1:*
2: pir2:*
3: pir3:*
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T00257
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hypothetical prote adhalin - golden h splicing factor SF hypothetical prote hypothetical prote op protein - Kenne protein tyrosine kinase reglutamic acid-rich hypothetical prote sulfated surface g hypothetical prote Fc gamma (19G) rectegument protein tyrothetical protein protein famma-glutamyl car hypothetical protein famma-glutamyl car hypothetical protein hypothetical protein fransactivator EBN hypothetical protein hypothetical protein for epsilon-chain -
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flt3 ligand isofor
hypothetical prote
74K alpha trans-in
                                                                                                                                                                                                                                                                                                                                    Description
                                                                                                                                                                                                                                                                                                                flt3 ligand - huma
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Qy 121 RFVQTNISRLIQETSEQLVALKPWITRQNFSRCLELQCQPDSSTLPPPWSPRPLEATAPT 180	QY 61 ASNLQDEELCGGLWRLVLAQRWMERLKTVAGSKMOGLLERVNTEIHFVTKCAFQPPPSCL 120	Qy 1 MTVLAPAMSPTTYLLLLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTV 60	Query Match 100.0%; Score 1242; DB 2; Length 235; Best Local Similarity 100.0%; Pred. No. 5.4e-99; Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	A;Molecule type: mRNA A;Residues: 1-71,'A',73-235 <han> A;Cross-references: GB:U04806; NID:g483844; PIDN:AAA17999.1; PID:g483845 A;Note: the authors translated the codon AGT for residue 25 as Met C;Genetics: A;Introns: 11/3; 48/3; 66/3; 114/3; 161/1; 220/3</han>	A;Title: Ligand for FLT3/FLK2 receptor tyrosine kinase regulates growth of haematopol A;Reference number: \$43290; MUID:94195428; PMID:8145851 A;Accession: \$43292 A;Status: preliminary	A;Residues: 1-235 <re2> A;Residues: 1-235 <re2> A;Cross-references: EMBL:U29874; NID:g1072036; PIDN:AAA90949.1; PID:g1072037 R;Hannum, C.; Culpepper, J.; Campbell, D.; McClanahan, T.; Zurawski, S.; Bazan, J.F.; felt, A.; Muench, M.; Kelner, G.; Namikawa, R.; Rennick, D.; Roncarolo, M.G.; Zlotnik Nature 368, 643-648, 1994</re2></re2>	A::Ille: Structural analysis of numan and murine rit3 ligand genomic loci. A:Reference number: I39075; MUID:96032581; PMID:7566977 A:Accession: I39075 A:Status: preliminary; translated from GB/EMBL/DDBJ A:Molegule type: DNA A:Molegule type: DNA	SSS SINGLE OF BUILD SAAAL SECTION SAAAAL SECTION SAAAA	A: Status: preliminary; translated from GB/EMBL/DDBJ A: Molecule type: mRNA A: Molecule type: mRNA	A; Title: Cloning of the human homologue of the murine flt3 ligand: a growth factor fo A; Reference number: I38440; MUID:94235842; PMID:8180375	<pre>C:Species: Homo sapiens (man) C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 01-Dec-2000 C:Accession: I38440; I39075; S43292 R;Lyman, S.D.; James, L.; Johnson, L.; Brasel, K.; de Vries, P.; Escobar, S.S.; Downe Blood 83, 2795-2801, 1994</pre>	RESULT 1 I38440 flt3 ligand - human	ALIGNMENTS	37 81.5 6.6 1119 2 T50995 rejacted to cytoske 38 81 6.5 196 2 B48232 cysteine-rich exte 40 81 6.5 209 2 A48232 cysteine-rich exte 41 81 6.5 294 2 AI2016 hypothetical prote 42 81 6.5 388 2 S15591 probable transposa 42 81 6.5 636 2 JW0047 class I cytokinase 44 80.5 6.5 1306 2 T13592 hypothetical prote hypothetical prote 45 80.5 6.5 1306 2 T13592 hypothetical prote	81.5 6.6 485 2 81.5 6.6 488 2

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S43293

FLT3/FLK2 ligand (clone S109) - human

C;Species: Homo sapiens (man)

C;Date: 20-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 17-Mar-1999

C;Date: 20-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 17-Mar-1999

C;Accession: S43293

R;Hannum, C.; Culpepper, J.; Campbell, D.; McClanahan, T.; 2urawski, S.; Ba.

R;Hannum, C.; Culpepper, J.; Campbell, D.; McClanahan, T.; 2urawski, S.; Ba.

R;Hannum, C.; Culpepper, J.; Campbell, D.; McClanahan, T.; 2urawski, S.; Ba.

R;Hannum, C.; Culpepper, J.; Campbell, D.; McClanahan, T.; 2urawski, S.; Ba.
                                                                                                                                                                                                                    A;Title: Structural analysis of human and murine flt3 ligand genomic loci A;Reference number: I39075; MUID:96032581; PMID:7566977 A;Accession: I39076
                                                                                                                                                                                                                                                                                                     RESULT 3
139076
Fit3 ligand alternatively spliced isoform - human
C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change
C;Accession: 139076
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A;Title: Ligand for FLT3/FLK2 receptor tyrosine kinase: A;Reference number: S43290; MUID:94195428; PMID:8145851
A;Accession: S43293
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                                                                                                                                                                     A;Status: preliminary; translated from GB/EMBL/DDBJA;Molecule type: DNAA;Residues: 1-178 <RES>
                                                                                                                                                                                                                                                                     R; Lyman, S.D.; Stocking, K.; Davison, B.; Oncogene 11, 1165-1172, 1995
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C;Genetics:
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Best Local
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Residues: 1-245 <HAN>
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MTVLAPAWSPTTYLLLLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APQP----
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                                                      Conservative
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                                                                                                                                                    EMBL: U29874; NID: g1072036; PIDN: AAA90950.1;
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                                                                    67.1%;
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73.0%;
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                                                                    Score 834; pred. No.
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Pred. No. 1.
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C; Keywords:
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A; Residues: 1-231 <LYM>
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                                                                                                                                                                                                                                                         Best
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                                                                                                                                                                                                                                       Matches
   178
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                                                                                                                                                                                                                                                       Local
   APTAPQPP---LLLLLLPVGLLLLAAAWCLHWQRTRRRTPRPGEQVPPVPSP
                                    LRFVQTNISHLLKDTCTQLLALKPCIGKACQNFSRCLEVQCQPDSSTLLPPRSPIALEAT
                                                                LRFVQTNISRLLQETSEQLVALKPWITR--QNFSRCLELQCQPDSSTLPPPWSPRPLEAT 177
                                                                                                   VAVNLQDEKHCKALWSLFLAQRWIEQLKTVAGSKMQTLLEDVNTEIHFVTSCTFQPLPEC
                                                                                                                                                                                                                                      163;
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fit3/fik-2 ligand precursor - mouse
C:Species: Mus musculus (house mouse)
C:Species: Nus musculus (house mouse)
C:Adate: 13-Jan-1995 #sequencervision 13-Jan-1995
C:Accession: A49265; 149347; 149346; 543290
R:Lyman, S.D.; James, L.; Vanden Bos, T.; de Vries,
D.; Williams, D.E.; Beckmann, M.P.
Cell 75, 1157-1167, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross references: GB:L23636; NID:g439441; PIDN:AAA39436.1; PID:g439442 R;Lyman, S.D.; Stocking, K.; Davison, B.; Fletcher, F.; Johnson, L.; Escc Oncogene 11, 1165-1172, 1955 R;Title: Structural analysis of human and murine flt3 ligand genomic loci A;Reference number: I39075; MUID:96032581; PMID:7566977 A;Accession: I49347
                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: mRNA
A;Residues: 1-197,'L',198-231 <HAN>
A;Experimental source: clone T110
A;Note: the sequence from Fig. 2c is inconsistent with that from Fig.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Title: Ligand for FLT3/FLK2 receptor tyrosine kinase regulates growth of haematopoi A;Reference number: $43290; MUID:94195428; PMID:8145851 A;Accession: $43290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:U29875; NID:g1072039; PIDN:AAA90951.1; PID:g1072040 R;Hannum, C.; Culpepper, J.; Campbell, D.; McClanahan, T.; Zurawski, S.; Bazz felt, A.; Muench, M.; Kelner, G.; Namikawa, R.; Rennick, D.; Roncarolo, M.G.; Nature 368, 643-648, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: DNA
A;Residues: 1-163,'G',165,'HYAG' <RES>
A;Cross-references: EMBL:U29875; NID:g1072039; PIDN:AAA90952.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Title: Molecular cloning of a ligand for the flt3/flk-2 tyrosine A; Reference number: A49265; MUID:94084791; PMID:7505204 A; Accession: A49265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-197, 'L', 198-231 <RE2>
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                                                                                                  1 MTVLAPAWSP-TTYLLLLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVT
VASNLQDEELCGGLWRLYLAQRWMERLKTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSC 119
                                                                          MTVLAPAWSPNSSLLLLLLLLSPCLRGTPDCYFSHSPISSNFKVKFRELTDHLLKDYPVT
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                                                                                                                                                                                                                                                                                                                11/3; 49/3; 67/3; 115/3; 164/1;
                                                                                                                                                                                                                                                                                        transmembrane
                                                                                                                                                                                  Conservative
                                                                                                                                                                                                        61.9%;
                                                                                                                                                                                                                                                                                  protein
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                                                                                                                                                                                                           Score 768.5; DB 2
Pred. No. 1.8e-58;
                                                                                                                                                                             Mismatches
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Roncarolo, M.G.; Zlotnik
                                                                                                                                                                                                                                      231;
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227

180

GSPDB:GN00021;

CESP:F

22;

Gaps

6

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C;Accession: S43291

C;Accession: S43291

C;Accession: S43291

C;Accession: S43291

C;Accession: C;Culpepper, J.; Campbell, D.; McClanahan, T.; Zurawski, S.; Bazan, J.F.; K; R;Hannum, C.; Culpepper, M.; Kelner, G.; Namikawa, R.; Rennick, D.; Roncarolo, M.G.; Zlotnik, J. Nature 368, 643-648, 1994

A;Title: Ligand for FLT3/FLK2 receptor tyrosine kinase regulates growth of haematopoiet: A;Reference number: S43290; MUID:94195428; PMID:8145851

A;Accession: S43291
                                                                                                                                                                                                                                                                                                                                                                                                                    R:Lyman, S.D.; James, L.; Escobar, S.; Downey, H.; de Vries, P. Oncogene 10, 149-157, 1995
A;Title: Identification of soluble and membrane-bound isoforms A;Reference number: I58343; MUID:95124710; PMID:7824267
A;Accession: I58343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Mus sp. (mouse)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 05-Nov-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FLT3/FLK2 ligand (clone T118) - mouse C:Species: Mus musculus (house mouse) C:Date: 20-Oct-1994 #sequence_revision
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A;Molecule type: mRNA
A;Residues: 1-220 <HAN>
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A;Residues: 1-220 <RES>
A;Cross-references: GB:S76459; NID:g913479; PIDN:AAB33069.1;
                                                                                                                                                                                                                                                                                                                                                                                                 A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Accession: I58343
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LREVQTNISRLLQETSEQLVALKPWITR--QNFSRCLELQCQPDSSTLPPPWSPRP----
                                                                                                                                                                                      MTVLAPAWSP-TTYLLLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVT 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATRLTATALLTVCPGLLLPLVGTSHMFFLPYFLSFLSS 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VASNLQDEELCGGLWRLVLAQRWMERLKTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSC 119
LRFVQTNISHLLKDTCTQLLALKPCIGKACQNFSRCLEVQCQPGNG------GPRAQHHG 174
                                                                              VAVNLQDEKHCKALWSLFLAQRWIEQLKTVAGSKMQTLLEDVNTEIHFVTSCTFQPLPEC
                                                                                                    VASNLQDEELCGGLWRLVLAQRWMERLKTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSC 119
                                                                                                                                                                 MTVLAPAWSPNSSLLLLLLLLSPCLRGTPDCYFSHSPISSNFKVKFRELTDHLLKDYPVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---LEATAPTAPOPPLLL-----LLLLPVGLLLLAA 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LRFVQTNISHLLKDTCTQLLALKPCIGKACQNFSRCLEVQCQPGNG-----GPRAQHHG
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                                                                                                                                                                                                                                                                     48.8%;
                                                                                                                                                                                                                                               ; Score 606.5; DB 2
; Pred. No. 1.3e-44;
18; Mismatches 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Score 606.5; DB 2;
; Pred. No. 1.3e-44;
18; Mismatches 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10-Nov-1995 #text_change 17-Mar-1999
                                                                                                                                                                                                                                                                                          DB 2; Length 220;
                                                                                                                                                                                                                                                 43;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein F54F12.1 - Caenorhabditis elegans C:Species: Caenorhabditis elegans C:pate: 15-Oct-1999 #sequence_revision 15-Oct-1999 #te: C:Accession: T22672 R:Barlow, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 7
T22672
                                                                                                                                                                                                                                               A;Gene: 12
C;Superfamily: herpesvirus 77K alpha trans-inducing protein
C;Keywords: trans-inducing protein; transcription regulatio
                                                                                                                                                                                                                                                                                                                                                                                            A;Title: The complete DNA sequence of varicella-zoster virus A;Reference number: A27345; MUID:86306657; PMID:3018124 A;Accession: C27342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   74K alpha trans-inducing protein - human herpesvirus 3
C;Species: human herpesvirus 3, varicella-zoster virus
C;Date: 30-Sep-1988 #sequence_revision 30-Sep-1988 #text_change 16-Jul-1999
C;Accession: C27342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: EMBL:Z81548; NID:e1062020; A;Experimental source: clone F54F12
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A; Residues: 1-661 <DAV>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                  A; Cross-references: EMBL: X04370;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Introns: 742/2; 826/1; 884/2; 922/3; 972/1; 1024/2; 1102/1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Gene: CESP:F54F12.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Genetics
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                                                                                                                                                                                                        Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           627 MDAVKAVDGTKYSSVIDALEKLSTMDLDFQKYKFKEAPATLKAMDL----FFASYASNLA 682
139
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                                    72 GLWRLVLAQRWMERLKTVAGSKMQGLLERVN----TEIHFVTKCAFQP---PPSCLRFV 123
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                                                                                                                     LLSSGLSGTQDCS----FQHSPISSDFAVKI--RELSDYLLQDYPVTVASNLQDEELCG- 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAVGGLLVVAIIGVILFFVFFQKKKKKEDKPDD--PPAPLP 781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LPVGLLLLAA----AWCLHWQRTRRRTPRPGEQVPPVPSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALRPQPTTSDPTAAAPVPIPNNKGSLNGNPSPSSPPLLPPVASSTPAATPEESNMLLYII 742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALKPWITRQNFSRCLELQCQPDSSTL---PPPWSPRPLEATAPTAP-----QPPLLLLLL 191
GLW-WVYENTYWQYLKYTTGAEVPVTSEKVNKKSKSTVLLFSSVVANKPISRHPFKSKVI 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATRLTATALLTVCPGLLLPLVGTSHMFFLPYFLSFLSS
                                                                              LTSPVLQSTERHSVLLGLHHNNVPESLVVSCMSNDVHDGFMQRYMETIQRCLDDLKLSGD
                                                                                                                                                              61; Conservative
                                                                                                                                                                                                                                             trans-inducing protein; transcription regulation
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23.6%; Pred. No. 8;
                                                                                                                                                                                  26.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Library,
                                                                                                                                                              29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33; Mismatches
                                                                                                                                                            Score 92; DB 1
Pred. No. 4.9;
29; Mismatches
                                                                                                                                                                                                                                                                                                                               NID:g59989; PIDN:CAA27895.1;
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                                                                                                                                                                                                        DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68;
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                                                                                                                                                                                                        Length 661;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                              Indels
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PID: 960001

36;

Gaps

11;

138

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adhalin - golden hamster

C; Species: Mesocricetus auratus (golden hamster)
C; Species: Mesocricetus auratus (golden hamster)
C; Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_chan
C; Accession: I48201
R; Roberds, S.L.; Campbell, K.P.
FEBS Lett. 364, 245-249, 1995
A;Title: Adhalin mRNA and cDNA sequence are normal in the car
A; Reference number: I48201; MUID:95278335; PMID:7758576
A; Accession: I48201
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-387 < RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Experimental source: clone C28D4
C;Genetics: A;Gene: CESP:C28D4.2
A;Gene: CESP:C28D4.2
A;Detron: 4
A;Intron: C.
                                                                                                                                                                                                                                                              RESULT 10
148201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein C28D4.2 - Caenorhabditis elegans
c;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T19543
R;McMurray, A.
submitted to the EMBL Data Library, November 1996
A;Reference number: Z19139
                                                                                                                                                                                                                                                                                                                                                                                В
                                                                                                                                                                                                                                                                                                                                                                                                           δÃ
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                                                 A; Cross-referen
C; Superfamily:
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A;Status: preliminary; translated
A;Molecule type: DNA
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A; Introns: 26/3; 72/3; 118/2; 169/1; 203/2; 240/2; 262/3; 298/3;
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Best Local S
Matches · 59
Best Local Similarity
                                                                  Cross-references: EMBL:U21677; NID:g726481; PIDN:AAA81645.1; PID:g726482
                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                  223
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                                                                                                                                                                                                                                                                                                                                                     230 LLLVE 234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                PKEPQ----
                                                                                                                                                                                                                                                                                                                                                                                                                                          VFTLLSERNLGPKMLGVFPGGRFEQFIPSRALQCLEISKPGLSKLIAPIVARVHTLDAPI 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TQDC-----SFQHS-PISSDFAVKIREL-SDYLLQDYPVTVASNLQDEELCGGLWRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GYGWMLWFLDVVD-----ARVCRHLKLQFRRIRGPRASV----IPDDLL
                                                                                                                                                                                                                                                                                                                         ITVAQ
                                                                                                                                                                                                                                                                                                                                                                                                           PTAPQPPLLLLLLPVGLLLLAAAWCLHWQRTRRRTP---RPGE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VKIEEF -- RIRAITGG - MSNLLFLVELPAH - LTPIQMEPEKALLRVHCQSDIDQLLSESV 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VLAQRWMERLKTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSCLR-FVQTNISRLLQET- 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTDCVDLKKVFSKFDSSAPISGEILFRARFLCAKYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QPPLLLLLLPVGLLLLAAAWCLHWQRTRRRTPRPGEQVPPVPSPQDLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NSDYRGICQELREALGAVQKYM---YFMR-----PDDPTNPSPDTRIRVQEIAAYTAT 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59;
                                                      mouse adhalin
                                                                                                                                                                                                                                                                                                                         271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -SEQLVALKPWITRQNFSRCLELQC----QPDSSTLPPPWSPR--PLEATA 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7.2%;
24.1%;
         7.2%;
                                                                                                                                                                                                                                                                                                                                                                                -TLQTARQWLERF----KKFPAGERPIEMYLTQAKVPKSDYPST 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 89.5; DB 2; Pred. No. 5.5;
         Score
Pred.
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         No.
         DB
4.8;
                       2;
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                                                                                                                                                                                                                   #text_change 20-Jun-2000
                     Length 387
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                                                                                                                                                                                                                                                                                                                                                                                                           -QVPPVPSPQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGAWRK 106
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                                                                                                                                            425
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A;Cross-references: GDB:9955873
A;Map position: 22q12.1-22qter
C;Superfamily: human splicing factor SF3a 120K chain; ubiquitin
C;Keywords: pre-mRNA splicing
F;714-790/Domain: ubiquitin homology <UBH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Homo sapiens (man)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
C;Accession: S60735; S60733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Genetics: A;Gene: GDB:SF3A120; PRP21; SAP114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: protein
A; Residues: 51-62;82-94;270-275;397-414;448-463 <KRA2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1-793 < KRA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Title: Mammalian splicing A; Reference number: S60733;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Accession: S60733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:X85237; NID:g899297; PIDN:CAA59494.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession: S60735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Kraemer, A.; Mulhauser, F.; Wersig, C.; Groening, K.; Bilbe, G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                splicing factor SF3a 120K chain - human
                                                                                                                                                                                                                                                                                                                                                                      Best Local
                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             111 CAFQPPP--SC--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          384 LDQH 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           324 MATSDIQMVHHCTIHGNTEELRQMAARREVPRPLSTLPMFNVRTGERLPPRVDSAQVPLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          260-272,
                                                                                                                                                                                                                                                                 LPPAPAPDEYLV--
                                                                                                                                                                                                                                                                                                       LAPAWSPTTYLLLLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASN 63
PEDDTKEKIGPSKPNEIPQQPPPPSSATNIPSSAPPITSVPRPPTMPPPVRTTVVSAVPV
                                                                                                                                VTKCA----FQPPPSCLRF---
                                                                                                                                                                                                                      LQDEELCGGLWRLVLAQRWME-RLKTV------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGLWELGELQLLNITSALDRGGRVPLPIEGRKEGVYIKVGSATPFSTCLKMVASPDSYAR 221
                                                                                   VEETAIGKKIGEEEIQKPEEKVTWDGHSGSMARTQQAAQANIT--LQEQIEAIHKAKGLV
                                                                                                                                                                           MQEHMRIG-----LLDPRWLEQRDRSIREKQSDDEVYAPGLDIESSLKQLAER-RTDIFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LVEH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GILEHDPFFCPPTEATGRDFLADALVTLLVPLLVALLL---TLLLAYIMCCRREGQLKRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SSTLPPPWSPRPLEAT----APTAPQPPLLLLLLLLPVGLLLLAAAWC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGLWRL-----VLAQRWMERLKTVAGSKMQGLLERVNTEIHFVT------K 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTYLLLLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASNLQDEELC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAQGQPPLLSCYDSLAPHFRVDWCNVSLVDKSVPEPLD------
                                                                                                                                                                                                                                                                                                                                                  67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               71;
                                                                                                                                                                                                                                                                                                                                                Similarity 22...
67; Conservative
                                        TRONE -- SRCLELQCQP ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1995
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                                                                                                                                                                                                                                                                                                                                                                  7.28; 22.38;
                                                                                                                                                                                                                                                               --LRFVQTNISRLLQETSEQLVALKPWITRQNFSRCLELQCQPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             factor SF3a120 MUID:96079958;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -LHWQRTRRRTPRP------
                                                                                                                                                                                                                                                                                                                                                34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26;
                                                                                                                                                                                                                                                                                                                                                                      Score 89;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                        -DSSTLP-----PPWSPRPLEAT----APT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           represents a PMID:7489498
                                                                                                                                                                                                                                                                                                                                                                  DB
                                                                                                                            -VQTNISRLLQETSEQLVALKPWI 145
                                                                                                                                                                                                                                                                                                                                                                                         1;
                                                                                                                                                                                                                                                                                                                                                  79;
                                                                                                                                                                                                                    ---AGSKMQGLLERVNTEIHF 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97;
                                                                                                                                                                                                                                                                                                                                                                                         Length
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                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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                                                                                                                                                                                                                                                                                                                                                  120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PID:g899298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  110;
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                                                                                                                                                                                                                                                                                                                                                Gaps
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  596
                                                                                     536
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                                          180
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A;Molecule type: mRNA
A;Residues: 1-1386 <SEK>
A;Cross-references: EMBL:AB007945; NID:g3413913; PIDN:BAA32321.1;
                                                                                                                                                                                                                                                       DNA Res. 4, 345-349, 1997
A;Title: Characterization of cDNA clones in size-fractionated cDNA libraries
A;Reference number: Z14085; MUID:98116662; PMID:9455484
                                                                                                                                                                                                                                                                                                       hypothetical protein KIAA0476 - human C;Species: Homo sapiens (man) C;Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 21-Jul-2000 C;Accession: T00257 R;Seki, N.; Ohira, M.; Nagase, T.; Ishikawa, K.; Miyajima, N.; Nakajima, D. DNA Res. 4, 345-349, 1997
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AB1990
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A;Cross-references: GB:BA000019; PIDN:BAB77837.1;
A;Experimental source: strain PCC 7120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R; Kaneko, T.; Nakamura, Y.; Wolk, C.P.;
Nakazaki, N.; Shimpo, S.; Sugimoto, M.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium An A;Reference number: AB1807; MUID:21595285; PMID:11759840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA Res. 8, 205-213, 2001
                                                                                                                                         A; Note:
                                                                                                                                                                        A; Experimental source: brain
                                                                                                                                                                                                                                      A; Status: preliminary; translated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein all1471 [imported] - Nostoc sp.
                                                                                                     Query Match
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Best Local 9
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       1104
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                                   21 SSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASNLQDEELC----GGLWRL
                                                                                       Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GLLLLAAAWCLHWQRTRRRTPRPGEQVPPVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PQSLKP--TKPIPPKLIEPKKSEDSKNLQRPRIPDSPKPIKNSQPEAPKPV--
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                                                                                    Similarity
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23.1%;
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                                                                      28;
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Pred. No. 3;
32; Mismatches
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                                                                 Pred. No. 23;
8; Mismatches
                                                                                                                                                                                                                                        from
                                                                                      Score 88.5;
Pred. No. 23;
   -GPVLSDRRLCLA--LDEPQLCNGHMGGASRR 1148
                                                                                                                                                                                                                                        GB/EMBL/DDBJ
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#text_change
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                                                                    63;
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30-Jun-2002
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                                                               A;Cross-references: GB:M24909; NID:g158507; PIDN:AAA28916.1; R;Jimenez, J.; Alphey, L.; Nurse, P.; Glover, D.M. EMBO J. 9, 3565-3571, 1990
A;Title: Complementation of fission yeast cdc2(ts) and cdc25. A;Reference number: S12008; MUID:91006056; PMID:2120044
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A; Molecule type: mRNA
A; Residues: 1-227, 'A', 229-479 <JIM>
A; Cross-references: EMBL: X57495; NI
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                                                 A; Accession:
                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-479 <EDG>
                                                                                                                                                                                     A; Reference number: A; Accession: A32290
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S12008

cdc2(ts) and cdc25(ts) mutants

identifies

PID: g158508

NID: 97706;

PIDN:CAA40732.1;

PID: 97707

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RESULT 15
A32290
R:Edgar, B.A.; O'Farrell, P. Cell 57, 177-187, 1989
A:Title: Genetic control of A:Reference number: A32290;
                                                                           protein-tyrosine-phosphatase (EC 3.1.3.48) cdc25 homolog C;Species: Drosophila melanogaster C;Date: 05-Oct-1989 #sequence_revision 25-Apr-1997 #text_C;Accession: A32290; S12008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Species: Kennedya yellow mosaic virus C; Date: 31-Dec-1993 #sequence_revision
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:D00637; NID:g221969; PIDN:BAA00531.1; A;Experimental source: strain Jervis Bay isolate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Title: The nucleotide sequence of the genomic RNA of kennedya A;Reference number: JQ0532; MUID:90218040; PMID:2324710 A;Accession: JQ0532
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A; Residues: 1-753 <DIN>
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J. Gen. Virol. 71, 925-931, 1990
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                                                                                                                                                                                                                                         PRKL 590
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41; Conservative
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      cell division MUID:89195217;
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                                                                                                                                                                                                                                                                                                                                                          ----VGLLLLAAAWCLHWQRTRRRTPRPGEQVPPVPS 226
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Pred. No.
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      patterns in the ; PMID:2702688
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                                                                                                     11-Jun-1999

    fruit fly

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A; Description: catalyzes hydrolysis of peptidyl-phosphotyrosine to peptidyl-tyrosine and A; Pathway: initiation of mitosis A; Pathway: initiation of mitosis A; Note: cdc25 activates the cdc2 protein kinase by dephosphorylating it C; Superfamily: protein-tyrosine-phosphatase string; cdc25-type protein-tyrosine-phosphatase; phosphoricine monoester hydrolase; C; Keywords: cell cycle control; mitosis; phosphoprotein; phosphoric monoester hydrolase; F; 252-456/Domain: cdc25-type protein-tyrosine-phosphatase homology <PTP>F; 379/Active site: Cys (phosphorysteine intermediate) #status predicted F; 385/Binding site: substrate phosphate (Arg) #status predicted
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A;Gene: FlyBase:stg
A;Cross:references: FlyBase:FBgn0003525
Search completed: May 27, 2003, 18:27:59
Job time: 22 secs
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Best Local Similarity 22.9
Matches 56; Conservative
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                                                                                                                                                                                                                                                                                                               147
                                                                                                                                                                                                                                                      174 LEATAPTA: -- POPPLILLLLLEPVGLLLLAAAWCLHWQRTRRRTPRPGEQVPPVPSPQDL 230
                                                                                                 243 VTISH 247
                                                                                                                                                       231 LLVEH 235
                                                                                                                                                                                                                                                                                                                                                                   118
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                                                                                                                                                                                                           200 ---TARDCFKRPEPP-----
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                                                                                                                                                                                                                                                                                                                                             SCLRFVQTNISRLLQETSEQLVALKP---WITRONFSRCLEL-QCQPDSSTLPPPWSPRP 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MGLLSPEGSPORFQIVROPKILPAMGVSS-----DHTPARS-FRI-FNSLSS------T 117
                                                                                                                                                                                                                                                                                                               SGLN-----SLISGQIKEQPAAKSPAGLSMRRPSVRRCLSMTESNTNSTTTPPPKTPE- 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7.0%; Score 87.5; Di
22.9%; Pred. No. 8.2;
ative 34; Mismatches
                                                                                                                                                                                                        -----ASANCSPIQSKRHRCATVEKENCPAPSPLSQ 242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          76;
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